STIC-Biotech/ChemLib

From:

Hamud, Fozia

Sent:

Thursday, August 04, 2005 4:29 PM

To:

STIC-Biotech/ChemLib

Subject:

sequence search 10/717,282

Please search 10/717,282, SEQ ID NO: 2 full length and residues 36-753; SEQ ID NO:1 full length and 86-234 against commercial data bases. thanks

Fozia Hamud **Patent Examiner** Remsen 4D64 Mail Box: Remsen 4C70 (571) 272-0884 Art Unit 1647

STAFF USE ONLY Searcher:_

Searcher Phone: 2-Date Searcher Picked up:_ Date Completed:__

Searcher Prep/Rev. Time:_ Online Time:_

******** Type of Search

NA#:_ AA#:

_ SPDI: Interference: Oligomer: S/L:__

Encode/Transl: Structure#:__

__ Text: Inventor:____ Litigation:_

******** Vendors and cost where applicable

STN: DIALOG:

QUESTEL/ORBIT: LEXIS/NEXIS:

SEQUENCE SYSTEM: WWW/Internet:_ Other(Specify):_



AX364580 Sequence
AR459410 Mus muscu
AR594210 Mus muscu
AX364572 Sequence
AX364575 Sequence
AX364578 Sequence
AX364578 Sequence
AX364582 Sequence

AF459444 AF494210

AX364572 AX364575 AX364578 AX350981 CQ718300 AX364582

9

AX364582 Sequence
AR494209 Mus muscu
AR424804 Mus muscu
AR728204 Gallus ga
AA508679 Gallus ga
AC097358 Homo sapi
AC092050 Homo sapi
AC19550 Rattus no
AC125152 Mus muscu
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AR401232 Danio rer
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BC93642 Macaca fa
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AF494209 AF7278204 AY278204 GGA508679 AC097358 AC092050 AC110350 AC10232 AF364103 AF401232 CR386972 BC966804 AB093642 BV003753 AC1166803

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VPSSELSLPLMRGLSTDQTETSSLTESVSSSGLGEBEPPALPSKLLSSGSCKADLGC
RSYTDELHAVAPL"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0208259-A 1 31-JAN-2002;
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Sequence 1 from Patent W00208259.
AX364570
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Location/Qualifiers
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(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                  4708233 seqs, 24227607955 residues
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Listing first 45 summaries
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PAT 15-FEB-2002

linear

DNA

ALIGNMENTS

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score 2383; DB 6; Length 2383; red. No. 0; Mismatches 0; Indels 0; Gaps 0;	CGGCCACCGCCCACTCGGGGGCCGGCGGGCCGGGGGGCGGGAAC	AGCITCTGCTCCGTCTTCTT	TGGGGGTCGGGCG 180	OY 	GCTGTACAACATCACCTT	ACGC	CTTTG 	Qy	ACAG		CTTT	AACC 	C-C1	AGCA	Qy	ACAC		AACAAGAAAAGTGATGCATTATGCCTTAAAGCCAGTGCACTCCCCGTGGGGCCGGGCCCAT 1020 QY CAGAGCCGTGGCCATCACAGTGCCACTGGTAGTCATATCGCGATGCGACGCTTTCAC 1080
Query Match 100.0%; EBST Local Similarity 100.0%; FMatches 2383; Conservative 0;	1 CCGCCGCGCCACCGCCACCACCACCACCACTC		TACGGT TACGGT	181 CGCGCGGGCGCCGACACTGT	rerre rerre	CAAAT CAAAT		GTCCC 	GAAGT GAAGT	41 TAGCT 41 TAGCT				CGACCATGCAC	CGAAGGACCTT		**************************************	961 AACAAGAAAAGTGATGATTAT 1021 CAGAGCCGTGGCCATCACAGTG

121 TACGGTCAACGCCTCAACGCCTCGCAGCTGGGCCGCTGGGCGGGC) (J—(D	GTCCCCAGGGGCCTCCGCATCCAATTCCTGAAAGGATTTCGGGTAATACTGGAGGAGCT 48	481 GAAGTCGGAGGGAAGACAGTGCCAACAACTGATTCTAAAGGATCCGAAGCTCAACAG 540 541 TAGCTTCAAAAGAACTGGAATGCAATCTCAACCTTTCCTGAATATGAAATTTGAAACGGA 600 541 TAGCTTCAAAAGAACTGGAATGGAATCTCAACCTTTCCTGAATATGAAATTTGAAACGGA 600 541 TAGCTTCAAAAGAACTGGAATGGAATCTCAACCTTTCCTGAATATGAAATTTGAAACGGA 600	601 TTATTTCGTAAAGGTTGTCCCTTTTCCTTCCATTAAAAACGAAAGCAATTACCACCCTTT 660 	661 CTTCTTTAGAACCCGAGCCTGTGACCTGTTGTTACAGCCGGACAATCTAGCTTGTAAACC 720 	721 CTTCTGGAAGCTCGGAACCTGAACATCAGCCAGCATGGCTCGGACATGCAGGTGTCTT 780 	781 CGACCATGCACCACAACTTCGGCTTCCTTCTTCTTCTACCTAC	841 CGAAGGACCTTTCAAGCGAAAGACCTGTAAGCAGGAGCAAACTACAGAGACGACCAGCTG 900	901 CCTCCTTCAAATGTTTCTCCAGGGGATTATATAATTGAGCTGGTCGATGACACTAACAC 960 	961 AACAAGAAAAGTGATGCATTATGCCTTAAAGCCAGTGCACTCCCCGTGGGCCGGGCCCAT 1020	1021 CAGAGCCGTGGCCATCACAGTGCCACTGGTAGTCATATCGGCATTCGCGACGCTCTTCAC 1080 1021 CAGAGCCGTGGCCATCACAGTGCCATGGTAGTCATATCGCGATTCGCGACGCTTTCAC 1080	1081 TGTGATGTGCCGCBAGAAGCAACAAAAATATATATTCACATTTAGATGAAGAGGCTC 1140 		1201 CTTTCTCTGCTATTCCAGTAAAGATGGCCAGAATCACATGAATGTCGCTCCAGTGTTTCGC 1280
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/ CLOCAL SCALLS.
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      2281 GTCATGCAAAGCAGATCTTGGTTGCCGCAGCTACACTGATGAACTCCACGCGGCCGCCCC 2340
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STDQTETSSLTESVSSSSGLGEEEPPALPSKLLSSGSCKADLGCRSYTDELHAVAPL"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                            2383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="IL17RLM"
/note="contains a putative TIR domain and SH3 interaction
domain; similar to sef; hIL-17RLM-L; alternatively
                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 44.77)
Xiong, S., Zhao, O., Rong, Z., Huang, G., Huang, Y., Chen, P., Zhang, S., Liu, L. and Chang, Z.
Liu, L. and Chang, Z.
Hose Inhibits PC-12 Cell Differentiation by Interfering with Ras-Mitogen-activated Protein Kinase MAPK Signaling
J. Biol. Chem. 278 (50), 50273-50282 (2003)
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Xiong.S.O., Huang,G.R., Zhao,O.H., Chen,P.L., Rong,Z.L., Ye,X.Y.,
Chen,Y., Liu,L., Fu,X.Y. and Chang,Z.J.
Direct Submission
                                                                                                                                                                                                                                                                                                                          Submitted (22-MAR-2002) Tsinghua Institute of Genome Research, Department of Biological Sciences and Biotechnology, and School Medicine, Tsinghua University, Beijing 100084, P.R. China Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCGCCGCGCCACCGCCCACTCGGGGCTGGCCAGCGGCGGGGGGGCGGGGCGCAAGAGAAC
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Pred. No. 0;
0; Mismatches
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/organism="Homo sapiens"

/orge="mmon"

/ob_tref="taxon:9606"

/chromosome="3"
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/note="IL17RLM-L"
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Best Local Similarity 98.1%;
Matches 2337; Conservative
                                   Homo sapiens (human)
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Mammalian receptor proteins; related reagents and methods
Patent: WO 0190358-A 13 29-NOV-2001;
SCHERING CORPORATION (US)
Location/Qualifiers
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Pred. No. 0;
0; Mismatches
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           uses thereof
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/22. .>2235
                                                                                                                                                                                    93.0%; Score 2215.4;
97.9%; Pred. No. 0;
:ive 0; Mismatches
     Jing, S.
11-17 receptor like molecules and u
Patent: WO 0168859-A 1 20-SEP-2001;
Amgen Inc. (US)
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                             Location/Qualifiers
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CGGTCCCTATACGTCGCCATTTGCAACATGCACCAGTTTATTGACGAGGAGCCCGACTGG CCCTATATTGACGAGGAGCCCGACTGG CGGTCCCTATACGTCGCCATTTGCAACGACGAGCACCAGTTTATTGACGAGGAGCCCGACTGG
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                                                                                              GAGAAATTTGATTCGGGCTTGGTTTTAAATGATGTCCATGTGCAAACCAGGGCCTGAGAGT
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Submitted (Mis-2001) Genomics, DNAX Research Inc., 901

California Ave., Palo Alto, CA 94304, USA

Location/Qualifiers

1. .2724

/organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
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Homo sapiens IL-17RD mRNA, complete cds.
AF458067
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/product="unnamed"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                               1999 TCGTCTGTGCCCTCATCCGAGCTGTCTCTGCCACTGATGGAAGGACTCTCGACGAGCAG
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Direct Submission

Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Kazuaa-Kamatari, Kisarazu, Chiba 292-0812, Japan

Kazuaa-Kamatari, Kisarazu, Chiba 292-0812, Japan

(E-mail:genomics@hri.co.jp, Tel:81-438-52-3985)

NEDO human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; cDNA full insert sequencing:

Research Association for Biotechnology (RAB); cDNA library

construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,

HRI, and Biotechnology center, National Institute of Technology and

Evaluation; clone selection for full insert sequencing: HRI and

RAB; annotation: HRI and RAB.
                          Toblad, T., Nounta, Y., Toglya, S., Komai, F., Hara, R.,
Takeuchi, K., Arite, M., Imose, N., Musashino, K., Yuuki, H. Oshima, A.,
Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T.,
Shiohata, N., Sano, S., Moriya, S., Moriya, H., Ishina, H., Satoh, N., Takami, S.,
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Goto, Y., Shinizu, F., Wakebe, H., Hishigaki, H., Watanabe, T.,
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Complete sequencing and characterization of 21,243 full-length
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Kusano, J., Kanehori, K., Takahashi-Fujii, A.,
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I. (bases 1 to 4478)
Xiong, S., Zhao, Q., Rong, Z., Huang, G., Huang, Y., Chen, P., Zhang, S., Liu, L. and Chang, Z.
Hang, E., and Chang, Z.
Ras-Mitogen-activated Protein Kinase MAPK Signaling with Bas-Mitogen-activated Protein Kinase MAPK Signaling
J. Biol. Chem. 278 (50), 50273-50282 (2003)
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                                                                                                                                                                   Yong, S., Zhao, Q., Huang, G., Chen, P., Rong, Z., Ye, X., Chen, Y., Liu, L., Fu, X. and Chang, Z.

Direct Submission
Submitted (22-WAR-2002) Tsinghua Institute of Genome Research, Department of Biological Sciences and Biotechnology, and School Medicine, Tsinghua University, Beijing 100084, P.R. China
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                     523. .2310
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sapiens (human)
sapiens
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Best Local Similarity 98.6
Matches 2146; Conservative
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Direct Submission

Submitted (10-JUJ-2002) GSF, Institut fuer Bioinformatik MIPS,
Ingolsteadter Landstr. 1, 85764 Neuherberg, Germany
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by MediGenomix (Martinsried/Germany) within the CDNA
sequenced by Medical Bermany (Martinsried/Germany) within the CDNA
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                                                                                                                                                                                                                                                                                                                                                   HSMBUS220 2406 bp mRNA linear PRI 12-JUL-2002
Homo sapiens mRNA; cDNA DKFZp434L0320 (from clone DKFZp434L0320).
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                                                                 2078 CAGATCTTGGTTGCCGCAGCTACACTGATGAACTCCACGCGGTCGCCCCTTTGTAACAAA 2137
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PRESDPCLKYKBAAVLGATGPADSQHBSGHGGLDQDGBRRPALDGSAALQPLHTVKA
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PSKLLSSGSCKADLGCRSYTDELHAVAPL"
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Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
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                             CAGATCTTGGTTGCCGCAGCTACACTGATGAACTCCACGCGGTCGCCCCTTTGTAACAAA
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                                                                                                                                                                                                                2169
                                                                                                                                                      2383
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                                                                                                                                                      2352 ACGAAAGAGTCTAAGCATTGCCACTTTAGCTG
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                                                          ATTCCAGTAAAGATGGCCAGAATCACATGAATGTCGTCCAGTGTTTCGCCTACTTCCTCC 1271
                                                                                                                                                                                      AGGACTTCTGTGGCTGTGAGGTGGCTCTGGACCTGTGGGAAGACTTCAGCCTCTGTAGAG 1331
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2018 TGGGTGAGGAGGAACCTCCTTCCTTCCAAGCTCCTCTTTTGGGTCATGCAAG
                                                                                              ATTCCAGTAAAGATGGCCAGAATCACATGAATGTCGCCCCAGTGTTTCGCCTACTTCCTCC
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                                                                                                                        208 GAGGATGAAAGCGGCTGCCCGACCCCGGCTTTGTGTTGCTAATGAGGGAGTGGGGCCAGC
                                                                                                                                                       192 GTGGCTGAAAGTGTGACTGGACTACAGGCAATCCTGGCCTTGGCAGGGAGTGGGGCCAGC
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                                                            DB 9; Length 4490;
                                                                                         31; Indels
                                                          Score 2123.4;
Pred. No. 0;
/lab_host="DH10B"
/note="Vector: pBluescript"
                                                                                         0; Mismatches
                                                          89.1%;
98.6%;
                                                                                          Conservative
                                                                            Similarity
                                                                                            Matches 2142;
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 24308146. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs.remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (11-OCT-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) 12477932
                                                /mol_type="mRNA"
/db_xref="taxon:9606"
/dlone="IMAGE:48130907"
/tisbue_type="Teetis"
/clone_lib="NIH_MGC_97"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human and mouse cDNA sequences
                                                                                                           BC038369
BC038369.1 GI:23512250
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/ Lissue type="testes"
212 . .2335
// Inde="hSef-b" alternatively spliced"
// Codon start=1
                                                                                                                                                                                                                                                   AY489047 2364 bp mRNA linear PRI 12-FEB-2004
Homo sapiens SEF splice variant b mRNA, complete cds, alternatively
spliced.
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                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2364)

Preger, E., Ziv, I., Shabtay, A., Sher, I., Tsang, M., Dawid, I.B., Altuvia, Y. and Ron, D.

Altuvia, Y. and Ron, D.

Alternative splicing generates an isoform of the human Sef gene with altered subcellular localization and specificity

Proc. Natl. Acad. Sci. U.S.A. 101 (5), 1229-1234 (2004)
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2232 TCCTGCCCTTCCTTCCAAGCTCCTCTTCTGGGTCATGCAAAGCAGATCTTGGTTGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (27-NOV-2003) Biology, Technion, Israel Institute of
Technology, Haifa 32000, Israel
Location/Qualifiers
                                       CAGCTACACTGATGAACTCCACGCGGTCGCCCCTTTGTAACAAAACGAAAGAGTCTAAGC
                                                            2292 CAGCTACACTGATGAACTCCACGGGTCGCCCCTTTGTAACAAAACGAAAGAGTCTAAGC
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="3"
/map="3p14.3"
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SUMMARIES

		Description		Aba95031 Human cyt	Aba95033 Human cyt	Aba95035 Human cyt	Aas18134 Human DNA	Aas15346 DNA encod	Abk62082 Human cDN	Adb63275 Human cDN	Abx71363 Human tra	Aas09517 Human cDN	Aca89858 Human cDN	Aca64642 Human cDN	Ada43240 Human int	Ada49781 Human int	Ada26974 cDNA enco	Adb66908 cDNA enco	Aad63615 Human IL-	Adg87392 Human PRO	Adl16688 cDNA enco	Adl16649 cDNA enco	Adl71309 Human IL-	
COTTANTANTOC		ΙΩ		ABA95031	ABA95033	ABA95035	AAS18134	AAS15346	ABK62082	ADB63275	ABX71363	AAS09517	ACA89858	ACA64642	ADA43240	ADA49781	ADA26974	ADB66908	AAD63615	ADG87392	ADL16688	ADL16649	ADL71309 .	
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	æ	Query Match		100.0	7.66	96.1	93.1	93.0	90.6	89.3	89.3	87.0	87.0	87.0	87.0	87.0	87.0	87.0	87.0	87.0	87.0	87.0	87.0	
		Score		2383	2376.6	2289	2218.6	2215.4	2158.4	2128	2127.2	2074.2	2074.2	2074.2	2074.2	2074.2	2074.2	2074.2	2074.2	2074.2	2074.2	2074.2	2074.2	
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ALIGNMENTS

Cytokine receptor; Zcytor18; cell proliferation; antipsoriatic; human; pulmonary alveolar proteinosis; familial periodic fever; antitumour; erythroleukemia; chromosome 3p14.3; gene therapy; ds. Human cytokine receptor, Zcytor18 nucleotide sequence. /*tag= a /product= "Zcytor18" Location/Qualifiers 86. .2347 ABA95031 standard; DNA; 2383 BP. (first entry) WO200208259-A2 20-MAY-2002 Homo sapiens ABA95031; Key

31-JAN-2002.

Ğao 26-JUL-2000; 2000US-0220747P. Presnell SR, Kuestner RE, (ZYMO) ZYMOGENETICS INC. WPI; 2002-217048/27. P-PSDB; ABB07626.

23-JUL-2001; 2001WO-US023253.

8

New cytokine receptor polypeptide designated zcytor18, useful for inhibiting cell proliferation associated with psoriasis or tumor growth, and modulating immune system by binding to endogenous zcytor18 ligand.

Claim 5; Page 85-90; 119pp; English

The invention relates to an isolated cytokine receptor polypeptide

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designated Zcytor18. The Zcytor18 polypeptides can be used to inhibit cell proliferation associated with psoriasis or tumour growth. The encoding nucleic acids are useful for providing Zcytor18 in vivo by gene therapy techniques. Zcytor18 oligonucleotide probes are useful for in vivo diagnosis, and the Zcytor18 probes and primers can be used to detect and localize Zcytor18 gene expression in tissue samples. The probes are useful for in linkage-based testing gross aberrations in chromosome 3 in which Zcytor18 gene resides. The Zcytor18 polymucleotides can also be used in linkage-based testing of pulmonary alvoplar proteinosis, familial periodic fever and erythroleukemia, and erythroleukemia associated with polymorphisms of cytokine receptors. The present sequence represents a
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The invention relates to an isolated cytokine receptor polypeptide designated Zcytor18. The Zcytor18 polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with psoriasis or tumour growth. The encoding nucleic acids are useful for providing Zcytor18 in vivo by gene therapy techniques. Zcytor18 oligonucleotide probes are useful for invivo diagnosis, and the Zcytor18 probes and primers can be used to detect and localize Zcytor18 gross aberrations in chromosome 3 in which also useful for detecting gross aberrations in chromosome 3 in which linkage-based testing of pulmonary alveolar proteinosis, familial periodic fever and erythroleukemia, and erythroleukemia associated with human Zcytor18 variant nucleotide sequence represents a human Zcytor18 variant nucleotide sequence
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2002-217048/27 WPI; 2002-217048, P-PSDB; ABB07628

The invention relates to an isolated cytokine receptor polypeptide designated Zcytor18. The Zcytor18 polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with psoriasis or tumour growth. The cell proliferation associated with psoriasis or tumour growth. The cenceding nucleic acids are useful for providing Zcytor18 in vivo by gene therapy techniques. Zcytor18 oligonucleotide probes are useful for in civo diagnosis, and the Zcytor18 probes and primers can be used to detect and localize Zcytor18 gene expression in tissue samples. The probes are also useful for detecting gross aberrations in chromosome 3 in which Zcytor18 gene resides. The Zcytor18 polymucleotides can also be used in linkage-based testing of pulmonary alveolar proteinosis, familial periodic fever and erythroleukemia, and erythroleukemia associated with polymorphisms of cytokine receptors. The present sequence represents a human Zcytor18 splice variant nucleotide sequence New cytokine receptor polypeptide designated zcytor18, useful for inhibiting cell proliferation associated with psoriasis or tumor growth, and modulating immune system by binding to endogenous zcytor18 ligand. Claim 5; Page 102-106; 119pp; English

Sequence 2341 BP; 550 A; 668 C; 625 G; 498 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                          The invention relates to primate and rodent DNAX cytokine receptor subunit (DCRS) polypeptides and the polymucleotides encoding them. The receptors, or their portions may be useful as phosphate labelling enzymes to label general or specific substrates. The subunits may also be functional immunogens to elicit recognising antibodies, or antigens be used as an immunogen for the production of antisera or antibodies apable of binding antibodies. A combination, e.g., including a DCRS can be used as an immunogen for the production of antisera or antibodies capable of distinguishing between other cytokine receptor family members. A purified DCRS can also be used as a reagent to detect antibodies generated in response to the presence of elevated levels of expression, or immunological disorders which lead to antibody production to the endogenous receptor. This sequence represents cDNA encoding the human DCRSB polypeptide
                                                                                                                                         Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide useful for detecting antibodies generated in response to presence of increased protein levels or immunological disorders.
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Interleukin 17; hIL-17 receptor like protein; immunomodulatory; anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial; hepatic; anabolic; ancretic; anti-alzheimer's; anti-parkinsonian; anti-convulsant; anti-sakhmatic; dermatological; renal; osteopathic; vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological; hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease; bone disease; vascular disorder; eye disorder; cancer; human; ss.
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The invention describes novel nucleic acids encoding interleukin (IL) 17

receptor like polypeptides useful as vaccines and in gene therapy. These

convenient inflammatory, anti-diabetic, anti-microbial,

immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimar's, renal,

canti-parkinsonian, anti-convulsant, anti-alzheimar's, renal,

costeopathic, vascular, cytostatic, anti-leukaemic, anti-infermility and

costeopathic, vascular, cytostatic, anti-leukaemic, anti-infermility and

costeopathic, vascular, cytostatic, anti-leukaemic, anti-infermility and

coptubalmological activities. The IL-17 receptor like nucleic acids and

coptubalmological activities. The IL-17 receptor like nucleic acids and

coptubalmological activities. The IL-17 receptor like nucleic acids and

coptubalmological activities. The IL-17 receptor like nucleic acids and

coptubalmological activities. The IL-17 receptor like nucleic acids and

coptubalmological activity and treat diseases associated with

coptubalmological activity disease (e.g. inflammation, diabetes and

cransplant rejection), infections (e.g. hepatitis and septicaemia),

coptubalmological and disease, achexia and obesity), neuronal

dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),

coptubalmological and psoriasis), kidney disease (e.g. glomerulonephritis),

coptubalmological and acherosclerosis, cancers (e.g. infertility and

coptubalmological and alterosclerosis, cancers (e.g. infertility and

coptubalmological and alterosclerosis, cancers (e.g. infertility and

coptubalmological and alterosclerosis, cancers (e.g. infertility and

coptubalmological and alterosclerative therapy. The ILI7TIP may also be used as

contingens in the production of antibodies against the proteins and in

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psoriasis and glaucoma.
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note= "No stop codon given"
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The invention relates to a novel human secreted polypeptide having sequence 90% identical to the polypeptide sequences of LP105, LP061, C sequence 90% identical to the polypeptide sequences of LP105, LP061, LP234 (a), LP234 (b), LP253, LP218), LP251 (b), LP251 (b), LP253 (b), LP234 (b), LP253 (b), LP251 (b), LP253 (b)
                                                                                                                           Human; 88; gene; secreted protein; cancer; autoimmune disease; arthritis; osteoprosis; Alzheimer's disease; Parkinson's disease; meningitis; encephalitis; neoplasia; trauma; ischaemia; infarction; mania; stroke; cardiovascular disease; atherosclerosis; sepsis; anaemia; rhoumatoid arthritis; hypothyroidism; allergic response; liver failure; multiple sclerosis; haemorrhage; paranoia; obsessive compulsive disorder; autism; panic disorder; learning disability; feeding disorder; sleep pattern disorder; balance; perception; Thl-dependent insulitis; adult respiratory distress syndrome; ARDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel polypeptides and polynucleotides of secreted proteins useful for treating various diseases such as multiple sclerosis, cancer, autoimmune diseases, osteoporosis, Alzheimer's disease and Parkinson's disease.
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ABK62082 standard; cDNA; 4392

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 TTGCCGCAGCTACACTGATGAACTCCACGCGGTCGCCCCTTTGTAACAAAACGAAAGAGT
               TTGCCGCAGCTACACTGATGAACTCCCACGGGTCGCCCCTTTGTAACAAAACGAAAGAGT
                                                                                                                                                                                                                                                        Human; ss; gene; pharmaceutical; diagnostic; gene therapy; tissue regeneration; cell regeneration; membrane protein; signal transduction-related protein; transcription-related protein; osteoporosis; neurological disease; cancer; tumour.
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Otsuka K, Nagai K, Irie
M, Nagahari K, Masuho Y;
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Otsuka M,
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(REAS-) RES ASSOC BIOTECHNOLOGY.
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Yoshikawa T,
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encoding them can be used as indicators for diseases (e.g. osteoporosis, neurological diseases, cancer, tumours. The CDNA may be used to regulate the activity or expression of the encoded protein to treat diseases. The sequence presented is a CDNA of the invention. Note: Some of the sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office.
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Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    311
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                                                                                                                                                                                                                                                                                                                                                                                                                      gene; gene therapy; vaccine; disease treatment; detection;
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      AAATATATATACACATTTAGATGAAGAGGGCTCTGAGTCTTCCACATACACTGCAGCACT
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1178 GTTCCAAAGGTATGAAGTACT 1452 GAGGCTCGGGGAAAGGAGG 1238 GAGGCTCGGGGGAAAGGAGGGGGGGGGGGGGGGGGGGGG	AAS09517 standard; cDNA; 2319 BP. AAS09517;
ANSTER OF SEARSES BORSES BORSE	XX XX AA XX X
98 ATTGTACCACCTACTTGAATCCCAGGGGAAGCATGTGATTGCTGACCCCCAGGAATATCT 157 312 CCATCACCCCCTACTTGAATCCCAGGGGAATTGCGAGGGAATTGCTGAGGGGAATTGCTGAGGGGAATTGCTGAGGGAATTGCTGAGGGAATTGCTGAGGGAATTGCTGAGGGAATTGCTGAGGGAATTGCTGAGGGAATTGCTGAGGAATTGCAGGAATTGCTGAGGAATTGCTGAGGAATTGCTGAGGAATTGCAGGAATTGCAGGAATTGCAGGAATTGCTGAGGAATTGCAGGAAGGA	1118 AAGGCAGAGAGAGTCCACACACACACACCCCAGTTCATCATGTGTTT 1177 11392 GTTCCAAAGGTTCTTGTGGACAAGAACTACAAACAAAGGGGGTT 1177

Length 2319;

DB 4;

Score 2074.2;

87.0%;

4

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The sequence (DNA 154095-2998) encodes a PRO polypeptide (PRO20026) which is the human Interleukin 17 receptor, IL-17RH4. A composition containing ant Agonists to the PRO polypeptides or individual components are useful for treating a mammal with an immune related disease, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an idiopathic inflammatory myopathy, Sjogran's syndrome, systemic vasculitis, saccoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, a contact dermatitis, an allergic disease e.g. food hypersensitivity, asthma, a transplantation associated disease, or a chronic inflammatory
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Vandlen RL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel PRO polypeptides homologous to interleukin-17, useful for the diagnosis and treatment of immune related disease e.g. rheumatoid arthritis and diabetes.
                                                                                                                 88;
                                                                                                      Human, Interleukin-17 receptor; IL-17RH4; agonist; antagonist; PRO20026; DNA 154095-2998; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; diabetes mellitus; allergic disease; aethma; demyelinating disease; degenerative cartilaginous disorder; transplantation associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Filvaroff E, Fong S, Goddard A, Godowski PJ,
LL, Li H, Hillan KJ, Tumas D, Van Lookeren M,
9 CK, Williams PM, Wood WI, Yansura DG;
                                                       Human cDNA encoding Interleukin 17 receptor, IL-17RH4
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2000US-00644848.
2000WO-US023328.
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2000US-0175481P.
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30-DEC-1999;
11-JAN-2000;
18-FEB-2000;
20-MAR-2000;
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585 A; 633 C; 602 G; 499 T; 0 U; 0 Other;

Sequence 2319 BP;

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Best Local Similarity 98.1
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2222 ACACTGATGAACTCCACGCGGTCGCCCCTTTGTAACAAAACGAAAGAGTCTAAGCATTGC 2281
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Gurney A, Li H, Hillan K, Tumas D, Vanlookeren M, Vandlen R;
Watanabe C, Williams PM, Wood WI, Yansura D;
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2000WG-US00541.
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99US-0138387P.
99US-0172096P.
99WO-US031274.
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2000US-0242837P.
2000US-0244072P.
                                                                                                                                                                Human cDNA encoding PRO20026
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87.0%; Score 2074.2;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 2125; Conservative 0; Mismatches 252 122 312 182 372 242 432 302

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Human; 88; gene; interleukin-17; IL-17; cytokine; T-lymphocyte; inflammatory cell; angiogenesis; gene therapy; immune-related disorder; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; Human cDNA encoding IL-17 family member, PRO20026. ВР ACA64642 standard; cDNA; 2319 (first entry)

17-JUN-2003

ACA64642;

ACA64642

sclerosis; idiopathic inflammatory myopathy; Sjogren's syndrome; sarcoidosis, autoimmune haemolytic anaemia; thyroiditis; psoriasis; diabetes mellitus; demyelinating disease; Guillain-Barre syndrome; autoimmune chronic active hepatitis; primary bilary cirrhosis; inflammatory bowel disease; immune-mediated skin disease; contact dermatitis; allergic disease; asthma; urticaria; eosinophilic pneumonia; idiopathic pulmonary fibrosis; transplantation-associated disease; graft-versus-host disease. 2000WO-US015264. 2000US-0213087P. 2000US-00644848. 99US-00311832. 99US-0172096P. 99WO-US031274. 2000US-0175481P. 2000WO-US004341. 2000WO-US005841. 2000US-0191007P. 2000WO-US030873. 2000US-0253646P. 2000WO-US007532 2000WO-US023328 2000US-0242837P 20-DEC-2000; 2000US-00747259 2000WO-US032678 US2003008815-A1. Homo sapiens. 18-FEB-2000; 02-MAR-2000; 21-MAR-2000; 21-MAR-2000; 02-JUN-2000; 20-JUN-2000; 22-AUG-2000; 24-AUG-2000; 01-DEC-2000; 11-JAN-2000; 10-NOV-2000; 14-MAY-1999; 23-DEC-1999; 28-NOV-2000 09-JAN-2003

New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO1031, PRO1122, PRO10272, useful in molecular biology, chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy.

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PJ, Grimaldi f, Vandlen R;

, Filvaroff E, Fong S, Goddard A, Godowski PJ AL, Li H, Hillan K, Tumas D, Vanlookeren M, be C, Williams PM, Wood WI, Yansura DG;

WPI; 2003-341350/32. P-PSDB; ABU72600

Watanabe Chen J,

(GETH) GENENTECH INC

Claim 2; Fig 17; 148pp; English.

The invention relates to an isolated nucleic acid comprising at least 80% sequence identity to 8 cDNA sequences encoding PRO polypeptides (or their extracellular domains) which are members of the interleukin-17 (IL-17) family of cytokines. Also included are expression vectors, host cells, the polypeptides (tased to a heterologous amino acid sequence, an anti-PRO cantibody, a composition comprising the above polypeptide (or its agonist or antagonist, or the antibody cited above) in combination with a carrier, determining the presence of a PRO polypeptide in a sample.

CC carrier, determining the presence of a PRO polypeptide in a sample.

CC carrier, determining the presence of a PRO polypeptide in a sample.

CC carrier, determining the presence of a RRO polypeptide in a sample.

CC dentifying a compound that mimics or inhibits the activity of the PRO polypeptides cited above, or a compound that inhibits the expression of a colypeptides cited above polypeptides, stimulating or inhibiting the control of T-lymphocytes, enhancing or decreasing the infilation of T-lymphocytes, enhancing or decreasing the infilation of infilammatory cells into a tissue of a mammal and inhibiting or stimulating angiogenesis induced by a PROLO31 polypeptide or its agonist in a mammal. The nucleic acid is useful in molecular biology, e.g. use as hybridisation probes, in chromosome and gene mapping, in generating the transgenic animals or knock-out animals which, in turn, generating either transgenic animals or knock-out animals which, in turn, casecul in the development and screening of therapeutically useful reagents. The PRO polypeptide or the antibody is used in preparing a condition responsive to the polypeptide or medicament for treating a condition responsive to the polypeptide or medicament for treating a condition responsive to the polypeptide or antibody, and in various diagnostic assays. For immune-related disorders,

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these may be systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathy, systemic selerosis, idiopathic inflammatory myopathy, Sjogran's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating disease of the central or peripheral nervous system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, chronic inflammatory demyelinating polyneuropathy, pepatobiliary disease, infectious or autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatorus hepatitis, sclerosing cholangitis, inflammatory courtionmune or immune-mediated skin disease, bullous skin disease, autoimmune or immune-mediated skin disease, bullous skin disease, contact dermatitis, psoriasis, allergic disease, atticaria, immunologic disease of the lung, eosinophilic pneumonias, curticaria, immunologic disease of the lung, eosinophilic pneumonias, cidopathic pulmonary fibrosis, hypersensitivity pneumonitis, cransplantation- associated disease, graft rejection or graft-versus-host disease. The composition is useful in treating the above-mentioned immune confilteration of T-lymphocytes, or increasing or inhibiting the present infilturation of inflammatory cells since a tissue of a mammal. The present confilteration of infilturation
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87.0%; Score 2074.2;

Best Local Similarity 98.1%; Pred. No. 0;

Matches 2125; Conservative 0; Mismatches
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14-MAY-1999; 99US-0131832P.
20-UN-1999; 99US-0138387P.
23-DEC-1999; 99US-0172096F.
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New interleukin 17 related mammalian cytokine polypeptide (IL-17E) polypeptide, useful for preparing composition for treating immune-related or inflammatory diseases, e.g. psoriasis, asthma, allergic rhinitis or
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                                           WPI; 2003-615512/58.
P-PSDB; ADA43241.
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Matches 2125; Conserv
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2101

2161 2312 2372

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Human; interleukin-17; IL-17; gene; ss; dermatological;
immunosuppressive; antiinflammatory; antitheumatic; antiarthritic;
osteopathic; antianaemic; antidiabetic; antithyroid; haemostatic;
whepatotropic; antipsoriatic; antiallergic; antiasthmatic; vasotropic;
gene therapy; immune related disorder; systemic lupus erythematosus;
rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
special arthritis; osteoarthritis; juvenile chronic arthritis;
spondyloarthropathy; systemic sclerosis;
idiopathic inflammatory myopathy; Sjogren's syndrome;
systemic vasculitis; autoimmune haemolytic anaemia;
autoimmune thrombocytopenia; thyroiditis; diabetes mellitus;
immune-mediated renal disease; demyelinating disease;
wherearie syndrome;
thyroiditis; diabetes mellitus;
inflammatory demyelinating polyneuropathy; hepatobiliary disease;
whiplais; primary biliary cirrhosis; sclerosing cholangitis;
inflammatory bowel disease; gluten-sensitive enteropathy;
whippel's disease; skin disease; erythema multiforme; contact dermatitis;
atopic dermatitis; food hypersensitivity, urticaria;
eosinophilic pneumonia; didopathic pulmonary fibrosis;
whypersensitivity pneumonia; transplantation; graft rejection;
whypersensitivity pneumonia; transplantation; graft rejection;
CGGTGAAAGCCGGCAGCCCCTCGGACATGCCGCGGGACTCAGGCATCTATGACTCGTCTG
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                                                         CGGTGAAAGCCGGCAGCCCCTCGGACATGCCGCGGGCACTCAGGCATCTATGACTCGTCTG
                                                                                                                                                                                                              CGTCTTCCCTGACGGAGAGCGTGTCCTCCTCTTCAGGCCTGGGTGAGGAGGAACCTCCTG
                                                                                                                                   /*tag= a
/product="PRO20026"
/note="Interleukin-17 and interleukin-17 receptor
related protein"
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DB 9; Length 2319;

Score 2074.2; Pred. No. 0; 0; Mismatches

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Claim 130; Fig 17; 140pp; English.
         98US-0085579P.
98US-0113621P.
99WO-US005028.
99US-0130232P.
99US-0131022P.
                                              99WO-US010733.
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99US-0172096P.
99WO-US031274.
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28-NOV-2000; 2000US-0253646P.
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P-PSDB; ADA49782.
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02-MAR-2000;
21-MAR-2000;
21-MAR-2000;
02-JUN-2000;
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24-AUG-2000;
24-OCT-2000;
                            21-APR-1999;
26-APR-1999;
14-MAY-1999;
19-UN-1999;
09-UN-1999;
30-DEC-1999;
11-JAN-2000;
                                                                                                                                     26-OCT-2000;
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18-FEB-2000;
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determining the lack of responsiveness by the cell or expression gene. This sequence encodes a novel PRO polypeptide with sequence similarity to interleukin-17 and the interluekin-17 receptor.
                                                                                                                                                     Sequence 2319 BP; 585 A; 633 C; 602 G; 499 T; 0 U; 0 Other;
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98.1%;
                                                                                                                                                                                                                                                                                                                   Matches 2125; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel polypeptides having sequence similarity to interleukin-17 and interleukin-17 receptor protein useful for treating, diagnosing immune related disorders and treating degenerative cartilaginous disorder in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PJ, Grimaldi JC;
Starvovasnik MA;
Wood WI;
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932 841 992 1022 TATATTCACATTTAGATGAAGAGCTCTGAGTCTTCCACATACACTGCAGCACTCCCAA 1081

TATATTCACATTTAGATGAAGAGCTCTGAGTCTTCCACATACACTGCAGCACTCCCAA

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182 ATTGTACCACCTACTTGAATCCAGTGGGGAAGCATGTGATTGCTGACGCCCAGAATATCA

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The present invention relates to the isolation of novel human PRO
C polypeptides, and the polynucleotide sequences encoding them. The novel
ERO polypeptides are human interleukin 17 (hiL-17) homologues. The PRO
polypeptide and polynucleotide sequences are useful for diagnosing and
c treating disorders associated with the aberrant expression or activity of
treating disorders associated with the aberrant expression or activity of
c treating disorders include degenerative cartilaginous
c disorders and immune related diseases, such as systemic lupus
c erythematosis (SiE), rheumatoid arthritis, osteoarthritis, juvenile
c chronic arthritis, spondyloarthropathy, systemic sclerosis, an idiopathic
cinflammatory myopathy, 5jogren's syndrome, systemic vasculitis,
sarcoidosis, autoimmune hemolytic anaemia, autoimmune thrombocytopaenia,
c thyroiditis, diabetes mellitus, immune-mediated renal disease, a
demyelinating disease of the central or peripheral nervous system,
cidiopathic demyelinating polyneuropathy, disilain-Barre syndrome, a
chronic inflammatory demyelinating polyneuropathy, and hepatobiliary
disparations or antoimmune or antoimmune active honerities or reference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease, infectious or autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, bilary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, binflammatory bowel disease, gluten-sensitive enteropathy, Whipple's disease, an autoimmune or immune-mediated skin disease, a bullous skin disease, erythema multiforme, contact dermatitis, psoriasis, an allergic disease, asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity, urticaria, an immunologic disease of the lung, ensemblantation-associated disease, graft rejection or graft-versus-host-disease. The present sequence encodes a human PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated IL-17 nucleic acids and polypeptides, useful for diagnosing and treating disorders with aberrant expression or activity of the IL-17 polypeptide, such as degenerative cartilaginous and immune-related disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2319 BP; 585 A; 633 C; 602 G; 499 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen J, Filvaroff E, Fong S, French D, Goddard A, Grimaddi JC, Gurney AL, Hillan KJ, Hymowitz SG, Li Starovasnik MA, Tumas D, Van Lookeren M, Vandlen R, Williams PM, Wood WI, Yansura DG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Fig 17; 161pp; English.
          20-DEC-2000; 2000MC-US034956.

20-DEC-2000; 2000WC-US034956.

22-MAR-2001; 2001WC-US006520.

22-MAR-2001; 2001US-00814208.

10-MAY-2001; 2001US-00854208.

10-MAY-2001; 2001US-00854208.

10-MAY-2001; 2001US-00854208.

20-JUN-2001; 2001WC-US017600.

20-JUN-2001; 2001WC-US019692.

20-JUN-2001; 2001WC-US01966.

09-JUL-2001; 2001WC-US021066.

09-JUL-2001; 2001WC-US021056.

30-JUL-2001; 2001WS-US021056.
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                                                                                                                                                                                                                                                                                                                                      13-AUG-2001; 2001US-00929404.
16-AUG-2001; 2001US-00931836.
                                                                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC.
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Godowski PJ; H, Pan J; Watanabe CK;

ATTGTACCACCTACTTGAATCCAGTGGGGAAGCATGTGATTGCTGACGCCCAGAATATCA

AGGGAGTGGGGCCAGCCAGCAGAAACAGTGGGGCTGTACAACATCACCTTCAAATATGACA

3; Indels 39; Gaps

87.0%; Score 2074.2; DB 9; Length 2319;

Pred. No. 0; 0; Mismatches

98.18;

Matches 2125; Conservative

252

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312 122

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Local Similarity

Query Match

371

1412 1052 992 961 872 781 932 841 301 491 361 551 421 611 481 671 541 731 601 753 661 721 1022 TATATICACATITAGAIGAAGAGGCTCTGAGTCTTCCACATACACTGCAGCACTCCCAA TGGCTCTGGACCTGTGGGAAGACTTCAGCCTCTGTAGAGAAGGGCAGAGAGAATGGGTCA crossaaccreaacarcasccascarsscrossacarscassgrocrrosaccacscac AGGAGCAAACTACAGAGACGACCAGCTGCCTCCTTCAAAATGTTTCTCCAGGGGATTATA TAATTGAGCTGGTGGATGACACTAACACAAGAAAAGTGATGCATTATGCCTTAAAGC CAGTGCACTCCCCGTGGGCCGGGCCCATCAGAGCCGTGGCCATCACAGTGCCACTGGTAG CAGTGCACTCCCCGTGGGCCCGGCCCATCAGAGCCGTGGCCATCACACAGTGCCACTGGTAG TCATATCGGCATTCGCGACGCTCTTCACTGTGATGTGCCGCAAGAAGCAACAAGAAAATA 1082 GAGAGAGCTCCGGCCGCGGGCCGAAGGTCTTTCTCTGCTATTCCAGTAAAGATGGCCAGA 1233 ATCACATGAATGTCGTCCAGTGTTTCGCCTACTTCCTCCAGGACTTCTGTGGCTGTGAGG TCCAGAAGATCCACGAGTCCCAGTTCATCATTGTGGTTTGTTCCAAAGGTATGAAGTACT TCTTCTATCTTCACTACAAGCTCAAGCACGAAGGACCTTTCAAGCGAAAGACCTGTAAGC AGGAGCAAACTACAGAGATGACCAGCTGCCTCCAAAATGTTTCTCCCAGGGGATTATA TATATTCACATTTAGATGAAGAGCTCTGAGTCTTCCACATACACTGCAGCACTCCCAA 1173 GAGAGGCTCCGGCCGCGCCGAAGGTCTTTCTCTGCTATTCCAGTAAAGATGGCCAGA GAACTGGAATGGAATCTCAACCTTTCCTGAATATGAAATTTGAAACGGATTATTTGGTAA GAACTGGAATGGGAATCTCAACCTTTCCTGAATATGAAATTTGAAAGGGATTATTTGGTAA ccceaeccrereaccrerrerracaecceacaarcraecrieraaccrrereaaec CCCTCGGCATCGAATTCCTGAAAGGATTTCGGGTAATACTGGAGGAGCTGAAGTCGGAGG GAAGACAGTGCCAACAGCTGATTCTAAAGGATCCGAAGCAGCTCAACAGTAGCTTCAAAA AGGITGICCCITICCITICCATIAAAAACGAAAGCAATIACCACCCITICITITAGAA CCCGAGCCTGTGTTGTTACAGCCGGACAATCTAGCTTGTAAACCCTTCTGGAAGC CTCGGAACCTGAACATCAGCCA--------754 -GCATGGCTCGGACATGCAGGTGTCCTTCGACCATGCACCGCACAACTTCGGCTTCCGTT 1202 ' 1262 1142 1293 1353 782 1053 1113 242 302 482 542 732 602 662 722 873 933 993 902 432 492 362 552 422 612 672 813 셤 ð 셤 ð g g a 쉽. ò 용 ઠે 임 ሯ g ઠે 유 ò 셤 ò 셤 ò 셤 ò 셤 ઠે 음 8 유 ò 셤 ò ò ઠ 8

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Human; PRO polypeptide; interleukin-17; IL-17; IL-17 receptor; immune related disorder; systemic lupus erythematosus; SLE; rheumatoid arthritis; osteoarthritis; Siogren's syndrome; autoimmune haemolytic anaemia; diabetes mellitus; immune-mediated renal disease; demyellinating disease; nervous system; duillain-Barre syndrome; immune-mediated skin disease; food hypersenstitivity; graft-versus-host disease; r-1ymphocyte proliferation; inflammatory cell; immunosuppressive; antiinflammatory; antiirheumatic; antiarthritic; osteopathic; antianaemic; antidiabetic; nephrotropic; hepatotrophic; dermatological; antiallergic;
                                             cDNA encoding human PRO polypeptide #9.
                                                                                                                                                                                                     US2003054442-A1
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                           04-DEC-2003
        ADB66908;
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                   CCGCGGCGCTCAGCAAGTTTATCGCCGTCTACTTTGATTATTCCTGCGAGGGAGACGTCC
                                                                                              CCGGTATCCTAGACCTGAGTACCAAGTACAGACTCATGGACAATCTTCCTCAGCTCTGTT
                                                                                                                                     CCCACTTGCACTCCCGAGACCACGGCCTCCAGGAGCCGGGGCAGCACACGCGACAGGGCA
                                                                                                                                                                           GCAGAAGGAACTACTTCCGGAGCAAGTCAGGCCGGTCCCTATACGTCGCCATTTGCAACA
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                                                TCTTCCTGGTGGCGGTGTCAGCCATTGCCGAAAAGCTCCGCCAGGCCAAGCAGGAGTTCGT
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New secreted and transmembrane PRO polypeptides and nucleic acids, useful for treating immune related disorders, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, diabetes mellitus, or systemic
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Tumas D, Vanlookeren M, Vandlen R;
Wood WI, Yansura D;
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2000WS-0191007P.
2000WO-US007532.
2000WO-US015264.
2000US-0213807P.
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99US-0130232P.
99US-0131022P.
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99US-0134287P.
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2000WO-US005601.
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                             2001US-00908827
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Gurney A, Li H, Hillan K,
Watanabe CK, Williams PM,
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P-PSDB; ADB66909.
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02-MAR-2000;
21-MAR-2000;
21-MAR-2000;
02-JUN-2000;
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24-OCT-2000;
26-OCT-2000;
10-NOV-2000;
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18-FEB-2000;
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20-MAR-2003
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BP.

ADB66908 standard; cDNA; 2319

RESULT 15 ADB66908 ID ADB6

Sat

2; Fig 17; 154pp; English

The present invention relates to the isolation of novel human PRO polypeptides show sequence similarity to interleukin-17 (IL-17) and to polypeptides show sequence similarity to interleukin-17 (IL-17) and to the IL-17 receptor. The PRO polypeptides, agonists, antagonists and antibodies that specifically bind to the PRO polypeptides are useful for treating an immune related disorder in a mammal, such as systemic lupus trathmatosus (SIE), rheumatoid arthritis, osteoarthritis, juvanile chronic arthritis, spondylarthropathy, systemic sclerosis, idiopathic inflammatory myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, diabetes mellitus, immune—mediated arenal disease, demyelinating disease of the central or peripheral nervous system, Guillain-Barre syndrome, hepatobiliary or graft-versus-host disease. A composition comprising a PRO polypeptide, agonist, antagonist or antibody is useful for the treatment of an immune the proliferation of Inlammatory cells into a tissue. The present sequence encodes a human PRO polypeptide of the invention.

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872 311 181 371 241 431 611 481 671 541 731 601 753 661 721 781 301 491 361 551 421 TCTTCTATCTTCACTACAAGCTCAAGCACGAAGGACCTTTCAAGCGAAAGACCTGTAAGC CCCGAGCCTGTGACCTGTTACAGCCGGACAATCTAGCTTGTAAACCCTTCTGGAAGC GAACTGGAATGGAATCTCAACCTTTCCTGAATATGAAATTTGAAACGGATTATTTCGTAA CCCGAGCCTGTGACCTGTTGTTACAGCCGGACAATCTAGCTTGTAAACCCTTCTGGAAGC CTCGGAACCTGAACATCAGCCAGCATGGCTGGACATGCAGGTGTCCTTCGACCACGCAC -GCATGGCTCGGACATGCAGGTGTCCTTCGACCATGCACCGCACAACTTCGGCTTCCGTT AGGGAGTGGGGCCAGCCAGCAGAAACAGTGGGCTGTACAACATCACTTCAAATATGACA ATTGTACCACCTACTTGAATCCAGTGGGGAAGCATGTGATTGCTGACGCCCAGAATATCA CCATCAGCCAGTATGCTTGCCATGACCAAGTGGCAGTCACCATTCTTTGGTCCCCCAGGGG CCCTCGGCATCGAATTCCTGAAAGGATTTCGGGTAATACTGGAGGAGCTGAAGTCGGAGG cccrceecarceaarrccreaaecarrrceecraaracreeaecaecreaaerceeaec GAAGACAGTGCCAACAACTGATTCTAAAGGATCCGAAGCAGCTCAACAGTAGCTTCAAAA GAAGACAGTGCCAACAACTGATTCTAAAGGATCCGAAGCAGCTCAACAGTAGCTTCAAAA GAACTGGAATGGAATCTCAACCTTTCCTGAATATGAAATTTGAAACGGATTATTTCGTAA Gaps DB 10; Length 2319; 39; Indels 3; Score 2074.2; Pred. No. 0; 0; Mismatches Query Match 87.0%; Best Local Similarity 98.1%; Matches 2125; Conservative 482 542 602 662 722 612 672 732 813 252 122 312 182 372 432 302 492 552 754

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1352 1472 1112 1172 1321 1381 1621 1052 841 992 901 ATGATGTCATGTGCAAACCAGGGCCTGAGAGTGACTTCTGCCTAAAGGTAGAGGCGGCTG GCAGAAGGAACTACTTCCGGAGCAAGTCAGGCCGGTCCCTATACGTCGCCATTTGCAACA CTCCTCCACTGCGCTACCGGGAGCCAGTCTTGGAGAAATTTGATTCGGGCTTGGTTTTAA ATGATGTCATGTGCAAACCAGGCCTGAGAGTGACTTCTGCCTAAAGGTAGAGGCGGCTG TCTTCCTGGTGGCGGTGTCAGCCATTGCCGAAAAGCTCCGCCAGGCCAAGCAGAGTTCGT CCGGTATCCTAGACCTGAGTACCAAGTACAGACTCATGGACAATCTTCCTCAGCTCTGTT CCCACTTGCACTCCCGAGACCACGGCCTCCAGGAGCCGGGGCAGCACACGCGACAGGGCA GCAGAAGGAACTACTTCCGGAGCAAGTCAGGCCGGTCCCTATACGTCGCCATTTGCAACA CTCCTCCACTGCGCTACCGGGAGCCAGTCTTGGAGAAATTTGATTCGGGCTTGGTTTTAA 1082 GAGAGAGGCTCCGGCCGCGCCGAAGGTCTTTCTCTGCTATTCCAGTAAAGATGGCCAGA TTGTGGACAAGAAGAACTACAAACACAAAGGAGGTGGCCGAGGCTCGGGGAAAGGAGGAG TCTTCCTGGTGGCGGTGTCAGCCATTGCCGAAAAGCTCCGCCAGGCCAAGCAGAGTTCGT CCGGTATCCTAGACCTGAGTACCAAGTACAGACTCATGGACAATCTTCCTCAGCTCTGTT CAGTGCACTCCCCGTGGGCCGGGCCCATCAGAGCCGTGGCCATCACAGTGCCACTGGTAG CAGTGCACTCCCCGTGGGCCGGCCCATCAGAGCCGTGGCCATCACAGTGCCACTGGTAG TCATATCGGCATTCGCGACGCTCTTCACTGTGATGCCGCAAGAAGCCAACAAGAAAATA TATATICACATITIAGAIGAAGAGAGCICIGAGICTICCACATACACIGCAGCACTCCCAA GAGAGAGGCTCCGGCCGCCGGAAGGTCTTTCTCTGCTATTCCAGTAAAGATGGCCAGA ATCACATGAATGTCGTCCAGTGTTTCGCCTACTTCCTCCAGGACTTCTGTGGCTGTGAGG TCCAGAAGATCCACGAGTCCCAGTTCATCATTGTGGTTTGTTCCAAAGGTATGAAGTACT TAATTGAGCTGGTGGATGACACTAACACAAGAAAAGTGATGCATTATGCCTTAAAAGC 842 TAATTGAGCTGGTGGATGACACTAACACAAGAAAAGTGATGCATTATGCCTTAAAGC TGGCTCTGGACCTGGGGAAGACTTCAGCCTCTGTAGAGAAGAGGCAAGAGAAATGGGTCA 1382 1442 1502 1622 1773 1682 1833 1742 1802 962 1173 1233 1142 1293 1202 1353 1262 1413 1322 1473 1533 1593 1653 1713 1022 1562 1893 782 1053 1113 873 933 993 902

TTCTTGGGGCAACCGGACCGACTCCCAGCACGAGAGTCAGCATGGGGGCCTGGACC 2012	AAGACGGGGAGGCCCGGCCTGCCCTTGACGGTAGCGCCGCCCTGCAACCCCTGCTGCAGC 2072 	CGGTGAAAGCCGGCGCCCTCGGACATGCCGCGGACTCAGGCATCTATGACTCGTCTG 2132 	TGCCCTCATCCGAGCTGTCTCTGCCACTGATGGAAGGACTCTCGACGGACCAGACAGA	CGTCTTCCCTGACGGAGAGGTGTCCTCCTCTTCAGGCCTGGGTGAGGAAGGA	CCCTTCCTTCCAAGCTCCTCTTCTGGGTCATGCAAAGCAGATCTTGGTTGCCGCAGCT 2312	ACACTGATGAACTCCACGCGGTCGCCCCTTTGTAACAAAAGGAAGG	CACTITA 2379 CACTITA 2288	
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Sequence 200159,
Sequence 17379, A
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Sequence 125, App
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
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US-09-549-679-9
US-08-06-064A-1
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APPLICANT: WILLIAMS, V. TILLAMS, V. MILLAMS, APPLICANT: WOOD, William APPLICANT: WOOD, William APPLICANT: WOOD, William APPLICANT: WOOD, WILliam APPLICANT: WOOD, WILLIAMS, V. MILLAMS, V.
                             Sequence 3882, Ap
Sequence 1875, Ap
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Sequence 857, App
Sequence 3, Appl
Sequence 3, Appli
Sequence 2, Appli
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Sequence 5, Appli
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Sequence 1, Appli
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Sequence 10765, A
Sequence 10280, A
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US-09-489-039A-3665
US-09-489-039A-3882
US-09-489-039A-3882
US-09-902-540-1875
US-09-902-540-857
US-08-822-586-45
US-07-642-734C-3
US-08-439-009A-3
US-09-103-840A-2
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US-09-105-537-5
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Patent No. 6569645
GENERAL INFORMATION:
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Grimaldi, Christopher
Gurney, Austin
Li, Hanzhong
Hillan, Kenneth
Tumas, Daniel
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Williams, P.Mickey
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Filvaroff, Ellen
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87.0%; Score 2074.2;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 2125; Conservative 0; Mismatches
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1342 1462 1162 1282 1402 GCCTTAAAGCCAGTGCACTCCCCGTGGGCCGGGCCCATCAGAGCCGTGGCCATCACAGTG 1042 AAAGGAGAGCTCTTCCTGGTGGCGGTGTCAGCCATTGCCGAAAAGCTCCGCCAGGCCAAG 1522 662 782 902 962 302 362 422 982 482 242 802 862 922 542 903 ATGAAGTACTTTGTGGACAAGAAGAACTACAAACACAAAGAGGTGGCCGAGGCTGGGG CAGAGITCGTCCGCGCCCCCCAAGITTATCGCCGTCTACTTTGATTATTCCTGCGAG CAGAGITCGTCCGCGGGGCTCAGCAAGTTTATCGCCGTCTACTTTGATTATTTCCTGCGAG CAGCTCTGTTCCCACTTGCACTCCCGAGACCACGGCCTCCAGGAGCCGGGGCAGCACACG GGAGACGTCCCCGGTATCCTAGACCTGAGTACCAAGTACAGACTCATGGACAATCTTCCT GGAGACGTCCCCGGTATCCTAGACCTGAGTACCAAGTACAGACTCATGGACATCTTCCT 183 GACCTGTTGTTACAGCCGGACAATCTAGCTTGTAAACCCTTCTGGAAGCCTCGGAACCTG 363 ACCTGTAAGCAGGAGCAAACTACAGAGATGACCAGCTGCCTCCTTCAAAATGTTTCTCCA 923 GGGGATTATATAATTGAGCTGGTGGATGACACTAACACAACAAGAAAAGTGATGCATTAT 423 GGGGATTATATAAATTGAGCTGGTGGATGACACTAACACAACAAGAAAAGTGATGTATAT 483 GCCTTAAAGCCAGTGCACTCCCCGTGGGCCCGGGCCCATCAGAGCCGTGGCCATCACAGTG CAAGAAAATATATATTCACATTTAGATGAAGAGGCTCTGAGTCTTCCACATACACTGCA GATGGCCAGAATCACATGAATGTCGTCCAGTGTTTCGCCTACTTCCTCCAGGACTTCTGT GATGGCCAGAATCACATGAATGTCGTCCAGTTTTCGCCTACTTCCTCCAGGACTTCTGT GAATGGGTCATCCAGAAGATCCACGAGTCCCAGTTCATCATTGTGGTTTGTTCCAAAGGT 843 GAATGGGTCATCCAGAAGATCCAGGTCCCAGTTCATCATTGTGGTTTGTTCCAAAGGT ATGAAGTACTTTGTGGACAAGAAGTACTACAAACACAAAAGGAGGTGGCCGAGGCTCGGGG ACCTGTAAGCAGGAGCAAACTACAGAGACGACCAGCTGCCTTCAAAATGTTTCTCCA GGCTGTGAGGTGGTCTGGGACCTGTGGGAAGACTTCAGCCTCTGTAGAGAAAGGGCAGAGA TTTCCTTCCATTAAAAACGAAAGCAATTACCACCCTTTCTTCTTTAGAACCGGAGCCTGT GACCTGTTGTTACAGCCGGACAATCTAGCTTGTAAACCCTTGGAAGCCTCGGAACCTG

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Pred. No. 1.7e-09;
0; Mismatches 311;
                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MACH 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PERKINS, PATRICIA Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
                                             USSN 08/538,765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Human
STRAIN: IL-17 R (hCTLA8 receptor)
                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 06
FILING DATE: 7 AUGUST 1995
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                           TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: LENGTH: 3223 base pairs TYPE: nucleic acid STRANDEDNESS: single
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Matches 280; Conservative
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ORIGINAL SOURCE
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US-VESU-SAPAN-SAPAN-S

Sequence 9, Application US/08620694A

Patent No. 5869286

GENERAL INFORMATION:
APPLICANT: Pariggs, Melanie
APPLICANT: Pariggs, Melanie
APPLICANT: Pariggs, Melanie
APPLICANT: Parigos, Melanie
CORRESPONDENCES: 10

CORRESPONDENCES: 10

CORRESPONDENCES: 10

CONTRY: Gattle
STATE: WA

COUNTRY: USA

ZIP: 98101

CONFUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: Pappe Power Macintosh

COMPUTER: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Apple, Version 6.0.1

CURRENT APPLICATION NUMBER: US/08/620,694A

FILING DATE: 21 MARCH 1996
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US-09-022-696-9
Sequence 9, Application US/09022696
Patent No. 6072037
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
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OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,696
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE:
CLASSIFICATION:
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            1804 FGGACAGGTTCCGGGACTGGCAGGTCCGCTGTCCGACTGGAATGTGAAACCTCT 1863
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APPLICANT: Yao, Zhengbin
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
3.0%; Score 71.4; DB 3; Length 3223;
Best Local Similarity 46.4%; Pred. No. 1.7e-09;
Matches 280; Conservative 0; Mismatches 311; Indels 12
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,255
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FILING DATE:
CLASSIFICATION:
APPLICATION NUMBER: USSN 08/620,694
FILING DATE: 21 MARCH 1996
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
FILING DATE: 3 AUGUST 1995
APPLICATION DATA:
FILING DATE: 23 MARCH 1995
ATTORNEY/AGENT INFORMATION:
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ORGANISM: Human
STRAIN: IL-17 R (hCTLA8 receptor)
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REGISTRATION NUMBER: 34,695
REPERENCE/DOCKET NUMBER: 2617
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3223 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: USSN 60/052,525
FILING DATE: 27 NOVEMBER 1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2623-A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3223 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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TELEFAX: (206)
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Best Local Similarity 46.4;
Matches 280; Conservative
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93..2690
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ORGANISM: Human
IMMEDIATE SOURCE:
CLONE: IL-17R
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                   1864 ACT 1866
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LOCATION:
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Pred. No. 1.7e-09;
0; Mismatches 311; Indels 12;
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1356 AGAAGATCCACGAGTCCCAGTTC----
                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Parricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECHONE: (206)587-0430
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Human
STRAIN: IL-17 R (hCTLA8 receptor)
FEATURE:
                                                                                                                                                                                                      TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3223 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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US-09-022-696-9
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1384 GTCAGAAGCAGGAGGATGGTGGAGGAACTCTAAGATCATCGTCCTGTGCTCCGGGGGA 1443
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US-08-978-773-3

US-08-978-773-3

Sequence 3, Application US/08978773

Patent No. 6083906

PATENT NORMATION:
APPLICANT: Troutt, Anthony
TITLE OF INVENTION: Method of Regulating Nitric Oxide Production
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CTTY: Seattle
STATE: WA
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Pred. No. 1.7e-09;
0; Mismatches 311; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple dowerMacintosh
COMPUTER: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1
CURRENT APPLICATION DATA:
FILING DATE:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                   TOPOLOGY: line
MOLECULE TYPE: C
HYPOTHETICAL: NC
                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Hum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , NAME/KEY:
, LOCATION:
US-09-022-253-9
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   1404 TGAAGTACTTTGTGGACAAGAAGAACTACAAACACAAAGGAGGTGGCCGAGGCTCGGGGA 1463
                                                                                                                                                                                                                                                                                                                                                                                GAGACGTCCCCGGTATCCTAGACCTGAGTACCAAGTACAGACTCATGGACAATCTTCCTC 1643
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                                                                 1444 CĠCGCGCCAAGTGĠCCAGCCCTCCTGGGCCGGGGGCGCCTGTGCGGCTGCGCTGCGCTGCGACC
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APPLICANT: Spriggs, Melanie
APPLICANT: Spriggs, Milliam
TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17
CORRESPONDENCE: 10
CORRESPONDENCE ADDRESS:
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COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: MICROSOft Word for Apple, Version 6.0.1
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,253
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694
FILING DATE: 21-WARCH-1996
FILING DATE: 21-WARCH-1996
APPLICATION NUMBER: USSN 08/538,765
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REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/09022253
Patent No. 6096305
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
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CLASSIFICATION:
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1384 GTCAGAAGCAGGAGATGGTGGAGGGAACTCTAAGATCATCGTCCTGTGCTCCCGCGCA 1443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 71.4; DB 3; 1
Pred. No. 1.7e-09;
0; Mismatches 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Human
STRAIN: IL-17 R (hCTLA8 receptor)
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                         TELEFRX: (206)
TELEFRX: (206)
SEQUENCE CHARACTERISTICS:
LENGTH: 3223 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.0%;
TELEPHONE: (206)587-0430
TELEFAX: (206)
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Best Local Similarity
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APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Spriggs, Milliam
TITLE OF INVENTION: No. 6191104el Receptor That Binds IL-17
CORRESPONDENCE: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
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CLASSIPICATION
PRIOR APPLICATION DATA:
APPLICATION UNMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTONNEY, AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
"TELECOMMUNICATION INFORMATION:
"TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US/09/022,259
FILING DATE:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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46.4%; Pred. No. 1.7e-09;
tive 0; Mismatches 311; Indels 12;
             APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, william
TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,260
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ORIGINAL SOURCE:
ORGANISM: Human
STRAIN: IL-17 R (hCTLA8 receptor)
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
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REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08
FILING DATE: 23 MARCH 1995
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INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: LENGTH: 3223 base pairs TYPE: nucleic acid STRANDEDNESS: single
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Matches 280; Conserve
GENERAL INFORMATION:
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STREET: 51 C.
TTY: Seattle
                                                                                                                                                                                                                                USA
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                                                                                                                                                                                       CITY: Seatt
STATE: WA
COUNTRY: US
ZIP: 98101
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1464 AAGGAGAGCTCTTCCTGGTGGCGGTGTCAGCCATTGCCGAAAAGCTCCGCCAGGCCAAAGC 1523
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NUMBER OF SEQUENCES:
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46.4%; Pred. No. 1.7e-09;
tive 0; Mismatches 311; Indels
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Patent No. 6197525
                                                                                TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECTLE TYPE: CDNA to mRNA HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 46.4
Matches 280; Conservative
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LOCATION: 93..2693
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GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
APPLICANT: Fanslow, William
TITLE OP INVENTION: No. 6197525el Receptor That Binds IL-17

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1356 AGAAGATCCACGAGTCCCAGTTC-----ATCATTGTGGTTTGTTCCAAAGGTA 1403
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                                                                                                                                                                                                                                                  SYSTEM: Apple Operating System 7.5.5 Microsoft Word for Apple, Version 6.0.1
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APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
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STRAIN: IL-17 R (hCTLA8 receptor)
                                                                                                                                                                                                                                                                              SOFTWARE: Microsoft Word for Appl
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,257
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                            E: Floppy disk
Apple Power Macintosh
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
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NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHRAACTERISTICS: I.ENGTH: 3223 base pairs TYPE: nucleic acid
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Best Local Similarity 46.4
Matches 280; Conservative
                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93..2693
                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (206)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                              USA
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STRANDEDNESS:
                                                                                                                                                        ZIP: 98101
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US-09-022-257-9
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                                                                                                       STATE: Wi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1744 GGGAGCTGTCGGGGGACAACTACCTGCGGAGCCCGGGCGGCGGCAGCTCCGCGCCGCCC 1803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1384 GTCAGAAGCAGGAGATGGTGGAGGAAGCAACTCTAAGATCATCGTCCTGTGCTCCTCGGGCGCGCA 1443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1624 gegakértérérégacererregegesegesesésesérakésesérekarásakakarresass 1683
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Patent No. 586286

GENERAL INFORMATION:
APPLICANT: Yea, Zhengbin
APPLICANT: Fanslow, William
TITLE OF INVENTION:
NUMBER OF SEQUENCE: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Immunex Corporation
STREET: 51 University Street
COUNTY: Seatle
                                                                                                                                                                                                                                                               Length 3223;
                                                                                                                                                                                                                                                               Score 71.4; DB 4; Length 3 Pred. No. 1.7e-09; 0; Mismatches 311; Indels
                               (hCTLA8 receptor)
                                                                                                                                                                    9
                                                                                                                              LOCATION: 93..2693
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                      3.0%;
                                                                                                                                                                                                                                                                                                      46.48;
                                                                                                                                                                                                                                                               3.09
Best Local Similarity 46.49
Matches 280, Conservative
ORGANISM: Human
STRAIN: IL-17 R
                                                                                              NAME/KEY:
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                                                                  FEATURE:
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US-08-620-694A-1
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US-09-549-679-9
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   AGAGTTCGTCCGCGCGCCCTCAGCAGTTTATCGCCGTCTACTTTGATTATTCCTGCGAGG 1583
                                                                  AGAGGCCAGCCTGCTTCGGCACCTACGTAGTCTGCTACTTCAGCGAGGTCAGCTGTGACG 1623
                                                                                                                                     GAGACGTCCCCGGTATCCTAGACCTGGGTACCAAGTACAGACTCATGGACAATCTTCCTC 1643
                                                                                                                                                                                                    acaacárceceacergricasececeacecearacececicarcarasacaserresas 1683
                                                                                                                                                                                                                                                                          AGCTCTGTTCCCACTTGCACTCCCGAGACCACGGCCTCCAGGAGCCGGGGCAGCACACGC 1703
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COMPUTER: Apple Power Macintosh
COMPUTER: Apple Power Macintosh
COMPUTER: Microsoft Word for Apple, Version 6.0.1
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/549,679
FILING DATE: VUNKnown>
APPLICATION NUMBER: US/09/694
FILING DATE: VUNKnown>
APPLICATION NUMBER: US/09/694
FILING DATE: SJ MARCH 1995
ATTONNEY AGENT INFORMATION:
NAMM: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spriggs, Melanie
Fanelow, William
TITLE OF INVENTION: No. 6680057el Receptor That Binds
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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STREET: 51 University Street
CITY: Seattle
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SEQUENCE CHARACTERISTICS:
LENGTH: 3223 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Patent No. 6680057
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
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US-09-549-679-9
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Sequence 1, Application US/09022255
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STRANDEDNESS: single
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121..2715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98101
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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Pred. No. 0.00011;
0; Mismatches 169; Indels 0
                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694A
FILING DATE: 21 MARCH 1996
CLASSIFICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION: 435
FILING DATE: 23 MARCH 1995
CLASSIFICATION: 435
FILING DATE: 34 MARCH 1995
CLASSIFICATION: A35
FILING DATE: 34 MARCH 1995
CLASSIFICATION: A35
FILING DATE: 34 MARCH 1995
CLASSIFICATION: A35
FILING DATE: CANNUMBER: 2617-B
RECHERNEL/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 48.0%;
Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Mouse
STRAIN: HVS13 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
121..2715
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ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-620-694A-1
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RESULT 13 US-09-022-255-1

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1683 AGGAGCCGGGGCACACGCGACAGGCAGCAGAAGGAACTACTTCCGGAGCAAGTCAG 1742
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Patent No. 6072033
GENERAL INFORMATION:
APPLICANT: Yeo, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 607203381 Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
Invention
Correspondence Address Corporation
Invention
ADDRESSEE: Immunex Corporation
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                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Microsoft Word for Apple, Version 6.0.1 CURRENT APPLICATION DATA:
FILING NAMES: US/09/022 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 54.6; DB 3;
Pred. No. 0.00011;
0; Mismatches 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: USSN 08/620,694
APPLICATION NUMBER: USSN 08/538,765
APPLICATION DATE: 7 AUGUST 1995
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           E: Floppy disk
Apple Power Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34.695
REFERENCE/DOCKET NUMBER: 261
TELECOMMUNICATION INFORMATION:
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MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3288 base pairs
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Best Local Similarity 48.0°
Matches 156; Congervative
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1640 TCAGTGGCATCTGTAGTGAGAGATGTCCCCGACCTCTTCAACATCACCTCCAGGTACC 1699
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                      1503 AAAAGCTCCGCCAGGCCAAGCAGAGTTCGTCCGCGCGCTCAGCAAGTTTATCGCCGTCT 1562
                                                            1580 Acardaricerdecadacerreadadeceadecerderregeadeceraderregerace 1639
                                                                                                          1563 ACTITGALTATICCTGCGAGGGAGACGICCCGGTATCCTAGACCTGAGTACCAAGTACA 1622
                                                                                                                                                                                             1623 GACTCATGGACAATCTTCCTCAGCTCTGTTCCCACTTGCACTCCCGAGACCACGCCTCC 1682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Troutt, Anthony
TITLE OF INVENTION: Method of Regulating Nitric Oxide Production
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIE: 99101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple PowerMacintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOCTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/052,525
FILING DATE: 27 NOVEMBER 1996
CLASSIFCATION: 530
ATTORNEY, AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2623-A
TELECOMUNICATION INFORMATION:
TELECHNONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1803 GGTTCGAAAAGCAGTTCGTTCCCTT 1827
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STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08978773
Patent No. 6083906
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 3288 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
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ORGANISM: Mouse
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HYPOTHETICAL: 1
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US-08-978-773-1
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1743 GCCGGTCCCTATACGTCGCCATTTGCAACATGCACCAGTTTATTGACGAGGAGGCCCGACT 1802
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                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09022696
Patent No. 6072037
GENERAL INFORMATION:
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION:
NOWBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
COMPUTER: Apple Operating System 7.5.5
OPERATING SYSTEM: Apple Operating System 7.5.5
OPERATING SYSTEM: Apple Operating System 7.5.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY, FACENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) S87-0430
TELEFAX: (206)
                                                                                                                                                       1803 GGTTCGAAAAGCAGTTCGTTCCCTT 1827
                                                                                                                                                                                               1880 GGTTCGAGCGTGAGAACCTCTGCTT 1904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE:
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INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3288 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Matches 156; Conservative
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2.3%; Score 54.6; DB 3; Length 3288;
Best Local Similarity 48.0%; Pred. No. 0.00011;
Matches 156; Conservative 0; Mismatches 169; Indels 0; Gaps
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Query Match
Best Local Similarity 93.7%; Pred. No. 0;
Matches 1676; Conservative 0; Mismatches 1; Indels 111; Gaps

ORIGIN

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AY408491 1674 bp DNA linear GSS 12-DEC-2003 Mus musculus HCM3241 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

AX408491
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 Rockville, MD 20850, USA
This sequence was made by sequencing gethem based on alignment.

Location/Qualifiers
1..1677
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db xref="taxon:9598"
<1...>1677
/locus_tag="HCM3241"
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  Mus musculus Eukarota; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Criurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 1674)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, B., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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                                                                                                                               Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Clark, A.G., Glanowski, S., Nielson, R., Tu, F., Murphy, B., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M. Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  980 TATGCCTTAAAGCCAGTGCACTCCCCGTGGGCCGGGCCCATCAGAGCCGTGGCCATCACA
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                                                                                                     Science 302 (5652), 1960-1963 (2003)
14671302
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/organism="Mus musculus"
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                                                                                                                                                                                                                                                                              /mol_type="genomic DNA'
/db_xref="taxon:10090"
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/locus tag="HCM3241"
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Best Local Similarity
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1459 1519 1579 1639 1699 1759 1143 1820 GIICCCIICCAICCICCACCICCACTGCGCTACCGGGAGCCAGICTIGGAGAAAITIGAITCG 1879 1263 1993 1323 2053 2113 1443 2173 2233 1563 1279 1339 970 CCTGAGCTCTGTGCCCCATCTGCACTCAGGAGAGCAGG-----AGGTGCTGGGTCAGCAC 1023 GCCATTTGCAACATGCACCAGTTTATTGACGAGGCCCCGACTGGTTCGAAAAGCAGTTC 1819 AGAGAATGGGTCATCCAGAAGATCCACGAGTCCCAGGTTCATTGTGGGTTTGTTCCAAA 1399 789 606 699 729 849 AAGCAGAGTTCGTCCGCGGCGCTCAGCAAGTTTATCGCCGTCTACTTTGATTATTCCTGC 1700 ACGCGACAGCAGCAGAAAGAAACTACTTCCGGAGCAAGTCAGGCCGGTCCCTATACGTC 1024 CCAGGCCACAGCAGCAGCAAGAACTACTTCCGGAGCAAATCGGGCCGCTCCCTGTATGTT GGCTTGGTTTTAAATGATGTCATGTGCAAACCAGGGCCTGAGAGTGACTTCTGCCTAAAG TCGACGGACCAGACAGAACGTCTTCCCTGACGGAGAGGCGTGTCCTCCTTCAGGCCTG AAAGATGGCCAGAATCACATGAATGTCGTCCAGTGTTTCGCCTACTTCCTCCAGGACTTC TGTGGCTGTGAGGTGGCTCTGGACCTGTGGGAAGACTTCAGCCTCTGTAGAGAAGGGCAG GGTATGAAGTACTTTGTGGACAAGAAGAACTACAAACACAAAGGAGGTGGCCGAGGCTCG GGGAAAGGAGCTCTTCCTGGTGGCGGTGTCAGCCATTGCCGAAAAGCTCCGCCAGGCC GAAGGGGATGTACCCTGCAGCCTGACCTGAGCACCAAGTACAAGCTCATGGACCACCTT 1084 GCCATTTGCAACATGCACCAGTTTATTGATGAGGAGCCTGACTGGTTTGAGAAGCAGTTT GTAGAGGCGGCTGTTCTTGGGGCAACCGGACCAGCGAC-----TCCCAGCACGAGAGT CAGCATGGGGGCCTGGACCAAGACGGGGCCCCGGCCTTGACGGTAGCGCCCC CTGCAACCCCTGCTGCACACGGTGAAAGCCGGCAGCCCCTCGGACATGCCGCGGGGACTCA GGCATCTATGACTCGTCTGTGCCCTCATCCGAGCTGTCTCTGCCACTGATGGAAGGACTC CCTCAGCTCTGTTCCCACTTGCACTCCCGAGACCACGGCCTCCAGGAGCCGGGGCAGCAC GCAGCACTCCCAAGAGAGAGGCTCCGGCCGCGGGCCGAAGGTCTTTCTCTGCTATTCCAGT GAGGGAGACGICCCCGGTATCCTAGACCTGAGTACCAAGTACAGACTCCATGGACAATCTT

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

To (Dassa 1 to 724)

Strong Europi, T., Suzuki, K., Sawazaki, T., Toki, D., Shinkai, H., Okumura, N., Hamaaihaa, N. and Awata, T.

PEDE (Pigg EST Data Explorer): construction of a database for ESTs derived from porcine full-length cDNA libraries

AL Nucleic Acids Res. 32 (1), D484-D488 (2004)

Animal Genome Laboratory, Genome Research Department

National Institute of Agrobiological Sciences

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Email: huenishi@affrc.go.jp

EST project with full-length enriched cDNA libraries carried out in Animal Genome Research Program (Japan) by National Institute of Agrobiological Sciences and STAFF-Institute

Single pass sequencing of clones derived from oligo-capped cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev stage="adult"
/clone_lib="full-length enriched swine cDNA library, adult
ovary"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vector sequences were eliminated by RepeatMasker version 2002/07/13
                                                                                                                                                                                                                                                                                                                                                                                                  BP154750 and linear EST 30-DEC-2003 BP154750 full-length enriched swine cDNA library, adult ovary Sus scrofa cDNA clone OVRM10115H10 5', mRNA sequence.
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                                                                         481 CATGCCGCGGGACTCAGGCATCTATGACTCGTCTGTGCCCTCATNCGAGCTGTCTCTGCC
361 CTCCCAGCACGAGAGTCAGCATGGGGGCCTGGACCAAGACGGGGAGGCCCGGCCTGCCCT
                                                                                                                                         2098 CATGCCGCGCGACTCAGGCATCTATGACTCGTCTCTGCCCTCATCCGAGCTGTCTCTCCC
                                              2038 TGACGGTAGCGCCCCCCCCCCCCTGCTGCACACGGTGAAAGCCGGCAGCCCCTCGGA
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                                                                                                                                                                                                                                       ACTGATGGAAGGACTCTCGACGGACCAGAAAGGTCTTCC 2200
                                                                                                                                                                                                                                                             /organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="OVRM10115H10"
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EST.
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Sus scrofa
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E 1 (bases 1 to 583)

Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S. Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

Genome Res. 14 (9), 1711-1718 (2004)

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Institute of Medical Science, University of Tokyo
1-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
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                                2293
                                                                                                                                                                                                                                                                                        BP275741 BP275741 Sugano cDNA library, kidney Homo sapiens cDNA clone KDN04362, mRNA sequence.
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                                                                1564 GGTGAGGAGCCCCCCTACCCTTCCAAGCTCTTTGCCTCTGGGGTGTCCA---GA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 gracagacricarggacaarcriccrcagcrcrgrrcccaccrgcacrcccagagaccacgg
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/mol_type="mRNA"
/db xref="taxon:9606"
/clone="kype="kidney"
/clone_lib="Sugano cDNA library, kidney"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 578.8; DB 5;
Pred. No. 3e-150;
0; Mismatches 3;
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BP275741.1 GI:52189473
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Best Local Similarity 99.5%;
Matches 580; Conservative
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Homo sapiens
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/d_ne="twdBE:745313"
/tissue_type="testis, pooled"
/lab.hofe="NHIOB TONA"
/lab.hofe="NHIOB TONA"
/clone lib="NHIH MGC 238"
/clone lib="NHIH MGC 238"
/clone lib="NHIH MGC 238"
/note="Organ: testis; vector: pExpress-1; Site_1: EcoRV;
Site_2: Not!; RNA obtained from testis tissue of 8 wk old animal. Tissues were snap-frozen and kept at -80C before RNA extraction and purification (Tri-reagent method). cDNA was primed using oligo-dT primer:
5-pGACTAGTTCTAGATCGCGAGCGCCC(T) 25-3' and cloned into the EcoRV/Not1 sites of pExpress-1. Size-selection >1.4kb
resulted in an average insert size of 1.9 kb. This primary library is normalized (non-normalized primary library is NIH MGC 237) and was constructed by Express Genomics
(FrederIck, MD)"
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Pred. No. 1.4e-119;
0; Mismatches 154;
                                                                                                     organism="Rattus norvegicus"
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Plate: LLAM15711 row: p column
High quality sequence stop: 689-
Location/Qualifiers
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/db_xref="taxon:10116"
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tes 589; Conservative 0
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NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Uppublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 RmlOAD7 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procuremnt: Howard Jacobs

CDNA Library Preparation: Express Genomics

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
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//organism="Homo sapiens"
//db_tref="embry"
//db_tref="treated hES cell line H7"
//clone lib="GAN PRENEU"
//clone lib="GA
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17000583090067 GRN_PRENEU Homo sapiens CDNA 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 462)

Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stanton, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation Nat. Biotechnol. 22 (6), 707-716 (2004) Contact: Brandenberger R
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230 Constitution Drive, Menlo Park, CA 94025, USA
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Fax: 650 473 760
Email: rbrandenberger@geron.com
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                                                                                                                       2034 CCCTTGACGGTAGCGCCGCCCTGCAACCCCTG
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Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (basea 1 to 640).

Rafata, A. Hiramoto, K., Hori, F., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Kouda, M., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shihaqawa, A., Takahashi, F., Tanaka, T., Tayami, M., Tagawa, A., Takahashi, F., Tanaka, T., Toya, T., Muramateu, M., and Hayashizaki, Y. Takeda, Y., Tanaka, T., Toya, T., Muramateu, M., and Hayashizaki, Y. Takeda, Y., Tanaka, T., Toya, T., Muramateu, M., and Hayashizaki, Y. Takeda, Y., Tanaka, T., Toya, T., Muramateu, M., and Hayashizaki, Y. Takeda, Y., Solinde, Hayashizaki, M. Pingublished (2001)

AL Ordeat: Yoshihide Hayashizaki

AL Contact: Yoshihide Hayashizaki

Indone, ESTE Chrome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute

Takeda, Y., Subiro-cho, Tsurumi-tw, Yokohama, Kanagawa 230-0045, Japan T-7-22 Suehizo-cho, Tsurumi-tw, Yokohama, Kanagawa 230-0045, Japan T-8-18-14-5-503-921

Email: genome-res@gec.riken.jp, URL:http://genome.gec.riken.jp/
Carninci, P., Shibata, Y., Hayateu, N., Sugahara, Y., Shibata, Y., Itoh, M., Konno, H., Okazaki, Y., Muramateu, M. and Hayashizaki, Y. Itoh, M., Konno, H., Okazaki, Y., Mayateu, Y., Izawa, M., Ohara, E., Matalization and subtraction of cap-trapper-selected convex Res. Ill-length cDM libraries for rapid discovery of new genes. Genome Res. Ill (10), 1617-1630 (2000)

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Sugahara, Y. and Hayashizaki, Y.

Aliawa, X., Fukuda, S., Hara,
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AAAAGCAGTTCGTTCCTTCCTCCTCCTCGCGTACCGGGAGCCAGTCTTGGAGA 1868
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Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
                                                 363 AAAAGCAGTTCGTTCCCTTCCATCCTCCTCCACTGCGCTACCGGAACCAGTCTTGGAGA
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/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="A830013G13"
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                                                                          adult male testis"
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                                                                         /clone lib="RIKEN full-length enriched, adult male testis
/note="Site 1: XhoI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
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                           tissue_type="testis"
'dev_stage="adult"
|lab_host="SOLR"
 clone="4931403M23'
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 84.2
Matches 510; Conservative
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Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Ouackenbush, J. and Keele, J.W. Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle denome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone lib="MARC 4BOV"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: SalI;
Library made from pooled tissue from day 20 and day 40
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Fax: 402 762 4396
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T..
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BU479802 717 bp mRNA linear EST 30-NOV-2002
603843254F1 CSEQREN22 Gallus gallus cDNA clone ChEST828k13 5', mRNA
sequence.
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1 (Dases 1 to 717)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E. Forgy, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A. Comprehensive Collection of Chicken cDNAs
                                                                                                                                                                               CAGATTACTTTGTCAAGATTGTGCCTTTTCCTTCCATTAAAAATGAAAGTAATTATCACC
                                                                                     131 GCCCAAGTTTTAAAAGAACAGGAATGGAATCCAATCCCTTTGCAATCTGAAGTTTGAAA
                                                                                                                                                                                                                                                                                                               251 CATTCTTTTCCGAACTCGGCCATGTGAATTATTGCTACAGCCAGAAACCTCATCTGCA
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                                                       537 ACAGTAGCTTCAAAAGAACTGGAATGGAATCTCAACCTTTCCTGAATATGAAATTTGAAA
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University of Manchester Institute of Science and Technology
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Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
1. 717
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Pasaianinae; Gallus.

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

A Comprehensive Collection of Chicken CDNAs

Curr., Biol. 12 (22), 1965-1969 (2002)
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BU221978 692 bp mRNA linear EST 25-NOV-200
603105617F1 CSEQCHN04 Gallus gallus cDNA clone ChEST44a6 5', mRNA
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University of Manchester Institute of Science and Technology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "mol type="mRNA"
'strain="White Leghorn, Hisex"
db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PO Box 88, Manchester, M60 1QD, UK Tel: 01612008930
Fax: 01612360409
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/organism="Gallus gallus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus (chicken)
Gallus gallus
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Mammalia, Eutheria; Rodentia; Sciurognachi; muridae; muridae; muse; Rokazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, T., Osato, N., Saito, R., Suzuki, H., Yangami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Riyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackehbush, J., Schriml, L.M., Kangalin, A., Marsuda, H., Batalov, S., Beisel, K., Brake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Gaasterland, T., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J. Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, B.D., Kanaj, A., Kawaji, H., Kawasawa, Y., Kedierski, R.M., King, B.L., Konagaya, A., Maltais, L., Marchiconi, L., Perteo, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Ravasi, T., Reed, J.C., Read, J.U., Ring, B.L., Konagaya, A., Schneider, C., Semple, C.A., Setou, M., Shinada, K., Sultana, R., Taylor, M.S., Tasadale, R.D., Tomita, M., Varagi, L., Wahlestedt, C., Wang, Y., Warcanabe, Y., Wang, L., Yang, L., Wahlestedt, C., Wang, Y., Warcanabe, Y., Yang, L., Yang, L., Yang, L., Wankawa, T., Fukwa, T., Yang, M., Yang, L., Yang, Y., Yang, Y.,
                                                                                                                                                                                                                                                                                                            667 bp mRNA linear BST 17-DEC-2002 BY726061 RIKEN full-length enriched, 2 cells egg Mus musculus CDNA clone B020034F22 5', mRNA sequence.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome-readgec.riken.jp, URL:http://genome.gec.riken.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
Imotani,K., Ishii,Y., Itoh, Kagawa,I., Kawai,J., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,
Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Direct Submission
602 -AGCAGAATTCAAATGACCTCTGCAAGTTCATTGCAGTCTACTTTGATTACTCCTGTGAG 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                            1583 GGAGACGTCCCCGGTATCCTAGACCTGAGTACCAA 1617
                                                                                                                       661 GGAGACATTCCTGGTATTCTGGATCTAAGTACCAA 695
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                                                                                                                                                                                                                                                                     RESULT 13
                                                                                                                                                                                                                                                                                                        BY726061
           셤
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                                                                                                                                                                                                                                                                                                /dev. stage="adult"
/lab_host="ballos"
/clone_lib="CSEQRBN22"
/clone_lib="CSEQRBN22"
/note="Vector: pBluescript II KS(+); Site_l: EcoRI;
Site_2: Not1; This normalized library was constructed from Site_2: Not1; This normalized library was constructed from 1 million independent clones. CDNA synthesis was initiated using an oligo(dr) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to Not1 adapters, digested with EcoRI, size-selected, and cloned into the Not1 and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCTGTGAGGTGGCTCTGGACCTGTGGGAAGACTTCAGCCTCTGTAGAGAAGGGCAGAGA 1342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1343 GAATGGGTCATCCAGAAGATCCACGAGTCCCAGTTCATCATTGTGTGTTTTCCAAAGGT 1402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCACTCCCAAGAGAGAGACTCCGGCCGCCGGAAGGTCTTTCTCTGCTATTCCAGTAAA 1222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1463 AAAGGAGGGTCTTCCTGGTGGCGGTGTCAGCCATTGCCGAAAAGCTCCGCCAGGCCAAG 1522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCACTGGTAGTCATATCGGCATTCGCGACGCTCTTCACTGTGATGTGCCGCAAGAAGCAA 1102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 GGTCTCCCTGTGGAAAGACTTCGCCCCGGCCAAAAGTATTCATCTGCTATTCCAGTAAA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 423 gaarggcricarraaaaaaaaaaargagricricagrirarcarcarrgrigrigcriccaaggga 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  543 AAAGGAGAACTCTTTCTGTTTTGCTGTGTTTACTGTTGCAGAGAAGCTTCGTCAAGCAAA- 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 GCACTAAAACCAGTACATTCTCCGTGGGCTGGACCAATAAGAGCTATTGCCATTACAGTC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 certragiticicartricgicartriccaacatricacagigaticateargicateargicaaaaagcag 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAAGAAAATATATATTCACATTTAGATGAAGAGAGCTCTGAGTCTTCCACATACACTGCA
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/tissue_type="Chondrocytes isolated from growth plate
cartilage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           923 GGGGATTATATATAGAGCTGGTGGATGACACTAACACAACAAGAAAAGTGATGCATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 caagagaararararrccarcragacgagagagacrcagaarcrrcagcrrargargc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1403 ATGAAGTACTTTGTGGACAAGAACTACAAACACAAAGGAGGTGGCCGAGGCTCGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 8.6e-106;
0; Mismatches 163;
                                                                                    strain="Layer and broiler"
           organism="Gallus gallus"
                                                                                                                           db xref="taxon:9031"
                                                                                                                                                             clone="ChEST828k13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 76.3%;
Matches 530; Conservative
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BQ830554 EST 15-SEP-2002 LL6in20509 AFT024-subtracted library Mus musculus CDNA 5' similar to Hypothetical human protein DKFZp434N1928, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=Torgan: Fetal Liver; Vector: Sport 1; Site_1: Sal I; Site_2: Not I; Two directionally cloned cDNA libraries were made from a hematopoietic stem cell-supporting stromal cell line (AFT024) and from a non-supporting stromal cell line (2018). Subtractive hybridization was performed by hybridization of the target, AFT024, single stranded cDNA library in pSport1 to biocinnlated RNA transcribed from the driver, 2018 cDNA library in pSport2 with inserts cloned in the complementary orientation. The AFT024-subtracted library contains 4.2x105 clones and is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: kmoore@molbio.princeton.edu
These ESTs are derived from a subtracted cDNA library enriched for
gene products expressed by a hematopoietic stem cell-supporting
stromal call libraryserse or T7.
Seq primer: M13Reverse or T7.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    beta-actin and enriched for transcripts specific to
AFT024. For detailed protocols and additional information
please see our website at
CACGGGCCTGTGACCTGTTGCAACCTGANCACTTGGCCTGNTAGCCTTTCTGGAAGC 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases I to 588)
Hackney, J. A., Charbord, P., Brunk, B. P., Stoeckert, C. J., Lemischka, I. R. and Moore, K. A. Anclecular profile of a hematopoietic stem cell niche Proc. Natl. Acad. Sci. U.S.A. 99 (20), 13061-13066 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       db xref="taxon:10090"
/tissue_type="Fetal Liver"
/cell_type="Stromal cell"
/cell_line="AFT024"
/dev_stage="Embryonic day 14-14.5"
/lab_host="DH108"
/clone_lib="AFT024-subtracted library"
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                                                                                                                633 CTCNGAACCTGAATATCAGCCAGCATGGTTCTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Moore, Kateri A.
Department of Molecular Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                         BQ830554
BQ830554.1 GI:22862622
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,609 258 2759
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Best Local 9
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ORGANISM
                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
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KEYWORDS
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                                                                                                                                                                                                                        RESULT 14
                                                                                                                                                                                                                                                 BQ830554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1711 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGAGATCCAAGAGCTCTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  252 AGGGAGTGGGGCCAGCCAGCAGAACAGTGGGCTGTACAACATCACCTTCAAATATGACA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       453 GGACTGGAATGGGAATCTCAGCCTTTCCTGAATATGAAATTTGAGACGGATTACTTTGTAA 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       312 ATTGTACCACCTACTTGAATCCAGTGGGGAAGCATGTGATTGCTGACGCCCAGAATATCA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCATCAGCCAGTATGCTTGCCATGACCAAGTGGCAGTCACCATTCTTTGGTCCCCAGGGG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone lib="RIKEN full-length enriched, 2 cells egg" /note="Site 1: Sal1; Site 2: BamH1; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   213 ACTGTACCACCTACTTGAATCCCGGCGGAAGCATGCGATTGCTGATGCTCAGAACATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATCAGCCAGTACGCTTGCCACGCGAGGTGGCAGTCACCATTCTTTGGTCCCCAGGG
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                                                                                                                                                                                                                                                                            prepare mouse tissues. Please visit our web site (http://genome.gsc.riken.go.jp) for
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87.8%; Pred. No. 1.3e-104;
ive 0; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/mol_type="mRNA"
/db xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="egg"
/dev_stage="2_cells"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone="B020034F22"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           constructed by Aaron M. Zorn.

Constructed by Aaron M. Zorn.

Constructed by Aaron M. Zorn.

Consolva was oligod Try primed from Sug of poly A+ RNA from stages 10-13

gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with

EcoRI at the.5' end and NotI at the 3' end.

Vector: pCS107; Site. I: EcoRI, Site. 2: NotI

Host: Escherichia coli XII- blue.

Location/Qualifiers
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia; Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus, Silurana.
1 (bases 1 to 886)
Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J.
Sanger Xenopus tropicalis EST project 2001 (11_2003)
                                                   61
AATTACCACCCTTTCTTTTTAGAACCCGAGCCTGTGACCTGTTGTTACAGCCGGACAAT
                                                                                                                                                                                                                                                                                                              AATTACCATCCCTTCTTCTTCAGAACACGGCCTGTGACCTGTTGTTACAACCTGACAAC
                                                                                                                                           ATGCAGGTGTCCTTCGACCATGCACCCCACACTTCGGCTTCCGTTTCTTCTATCTTCAC
                                                                                                                                                                                                           ATGCACGTGTCCTTCGACCATGCCCCGCAGAACTTCGGCTTCCGTGGCTTCCATGTTCTC
                                                                                                                                                                                                                                                TACAAGCTCAAGCACGAAGGACCTTTCAAGCGAAAGACCTGTAAAGCAGGAGCAAACTACA
                                                                                                                                                                                                                                                            GAGACGACCTGCCTCCTTCAAATGTTTCTCCAGGGGATTATATTGAGCTGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Croning MDR
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopius troppicalis EST project 2001
TROPICALIS_ESQUENCE ID: TGas082k14.q1kT7
Sequencing primer: T7
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BX750910
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AUTHORS
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JOURNAL
COMMENT
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                                                                                  /dev stage="gastrula (stages 10.5-12 mixed)"
//lab_host="Escherichia coli XL1-blue"
//clone lib="XGC-gastrula
//note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNĀ from stages
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
into pCS107 with EcoRI at the 5' end and NotI at the 3'
end."
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                                                                                                                                                                                                                                                                                                                                  17.3%; Score 411.6; DB 5; 67.5%; Pred. No. 2.4e-103; tive 0; Mismatches 279;
organism="Xenopus tropicalis"
                   /mol_type="mRNA"
/db xref="taxon:8364"
                                                                   /clone="TGas082k14"
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Search completed: August 11, 2005, 08:01:30 Job time : 8375.67 secs

AX364575 Sequence AX364582 Sequence AX364582 Sequence AX378204 Gallus ga AX603750 Sequence AX803750 Sequence Continuation (26 o AC111564 Dasypus n AC111564 Desypus n AC111564 Oryza sat AR005674 Oryza sat AR105862 Oryza sat AK105862 Oryza sat AK105862 Oryza sat AK06381 Oryza sat

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/ DEOTET 1164 "CAD23766.1"

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AAARBELCYANIGGYGEARNGLOLCSVFFTVNACLINGSQLAVAGGGSGRARGADTCGWRMK
AAARBELCYANIGGYGEARNGGLYNITFKYDNCTTYLAPVGKHYIADAQNITISQYAC

HDQVAVTILWSPGALGIEFLKGFRVILLEELKSEGRQCQOLILKOPROLLACKFFWTGWE
SQPFINKKETDYFWKVVPPPSIKORSNYHPPFRTRACDLLLQPDNILACKFFWRDRN
LNISQHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKKTCKGRQCTTETTGN
VSFGDY II BLYDDTNATRKWHYALKFVHSPWAGPIRAVAITVPLIVVISAPATLETUW
CRKKQQENIYSHLDBESSESSSTYTAALPRERLKPRPRFYFFLCXSSKYGGWNWNVVGCFA
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HKGGGRGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIANYFDVSCEGDVPGILLDL
STKYRLMDNLPQLCSHLHSRDHGLQFEGQHTRQGSRNYFRSKGRSLYVAICNHQF
IDEEPDWFEKQFVPFPPPLRYREPVLEKFDSGLVLANDWGKRGPESDFCLKVEAAVL
GATGPADSQHESQHGGLDQDGBARPALDGSAALQPLLHTVKAGSPSDMPRDSGIYDSS
VPSSELSLPLMEGLSTDQTETSSLTESVSSSSGLGBEEPPALPSKLLSSGSCKADLGC
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/codon_start=1
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Human cytckine receptor
Patent: WO 0208259-1 131-JAN-2002;
Zymodenetics, Inc. (US)
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1 .2383
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AX803750
AP006840_25
AC151564
AC134699
BX571965_35
CP000010_26
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Sequence 1 from Patent W00208259.
AX364570
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AX364573 Sequence
AX364576 Sequence
AX458067 Homo sapi
AX392973 Sequence
AK494208 Homo sapi
AC097358 Homo sapi
AC097358 Homo sapi
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AC125152 Mms muscu
AC124603 Mms muscu
AC116282 Rattus no
AC119550 Rattus no
AX364572 Sequence
                                                                                  August 16, 2005, 03:35:56; Search time 1906 Seconds (without alignments) 3787.947 Million cell updates/sec
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                                                                                                                                                           1 atggccccgtggctgcagct.....aaagcggctgcccgacccg
              GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                    4708233 segs, 24227607955 residues
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Maximum Match 100%
Listing first 45 summaries
                                                            - nucleic search, using sw model
                                                                                                                                  US-10-717-282-1_COPY_86_234
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Maximum DB
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PAT 15-FEB-2002

L18964 Human prote CQ716916 Sequence BC022016 Homo sapi AY328910 Oryza sat AX328999 Oryza sat AC026372 Homo sapi AC1223891 Homo sapi AC120538 Oryza sat AK108314 Oryza sat AK108314 Oryza sat

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BTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATTSCLLQNVSRGOYIIELVDDT
BESSESSTYTAAL.PRELIKPRRYFLCYSSKOGONHMVVVQCRAFLQDFCGGEVALD
LWEDFSLCREGQREWVIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGGRGSGKGELF
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SHLHSRDHGLQEPGQHTRQCSRRNYFRSKSGRSLYVATCNMHQFIDEEPDWFEKQFVP
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                                                                                               PAT 15-FEB-2002
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STDQTETSSLTESVSSSGLGEEBPPALPSKLLSSGSCKADLGCRSYTDELHAVAPL"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2724)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 6.3e-16;
0; Mismatches 10; Indels (
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Homo sapiens IL-17RD mRNA, complete cds.
AF458067
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Patent: WO 0208255A 7 31-JAN-2002;
ZymoGenetics, Inc. (US)
Location/Qualifiers
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206 TGGAGGATGAAAGCGGCTGCCCGACCCCG 234
                                                                                         2341 bp
Sequence 7 from Patent W00208259.
AX364576
AX364576.1 GI:18696536
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93.0%;
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KRKQDENIYSHLDEBSESSTYTAALBRENLERPRKVPLCYSSKDGOPHDNVYQCFA
YFLQDFCGEBVALDLWEDFSLCKEGOREWYLOKIHESGFIIVUCSKGMKYFVDKKOYF
HKGGRGGGKGELFLVAVSAIREKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILDL
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IDEEDDWFREXCFVPFHPPPLEXYREPULKFDSGLTUNDWYGKRGPESDFCLKVFAAVL
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VPSSELSLPLMRGLSQDGTETSSLTESVSSSSGLGEEEPPALPSKLLSSGSCKADLGC
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SQPFLNMKFETDYFVKVVPFPSIKNESNYHPFFFRTRACDLILQPDNLACKPFWKPRN
LNISQHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTEMTSCLLQN
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                                                                                                                     145
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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      Length 2383;
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  100.0%; Score 149; DB 6;
100.0%; Pred. No. 2.5e-20;
ive 0; Mismatches 0;
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protein_id="CAD23767.1"
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Sequence 4 from Patent WO0208259.
AX364573
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Query Match
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Matches 149, Conservative
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Matches 149; Conservative
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/gene="IL17RLM"
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GPASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVTIMSPGA
LGIEPLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFKRTGMESQPFLNMKFETDYF
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                     Gilbert, J.M. and Gorman, D.M.
Gilbert, J.M. and Gorman, D.M.
Birect Submission
Submitsed (13-DEC-2001) Genomics, DNAX Research Inc., 901
California Ave., Palo Alto, CA 94304, USA
Location/Qualifiers
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     Identification of novel IL-17 related receptors Unpublished
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Patent: WO 0214358-A 15 21-FEB-2002;
ELI LILLY AND COMPANY (US)
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/db xref="taxon:9606"
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Sequence 15 from Patent W00214358.
AX392973
                                                                                                                                                                                        'note="cytokine receptor"
                                                                                                                            /organism="Homo sapiens"
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1. _2220
                                                                                                                                                                                                                /product="IL-17RD"
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/db_xref="G1:21779863"
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/organism="Homo sapiens"
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Location/Qualifiers
 and Gorman, D.M
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Matches 133; Conservative
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CITED AT 1012 "MAPPHILDICS VEFTVNACINGS OLAVAGGS GRARGADTCGWRCY GPASRNSGLYNITEKYDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVTILMSEGA GEASRNSGLYNITEKYDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVTILMSEGGA LIGIBFLKGFRYLILELKSEGRQCQUILKDFRQLINSFRKTARSGOPFRAMKFRINKEFDYF VKVPFPSIKNESNYHPFFRRACHOLLLQDPDILACKFFWKPRNINISQHGSDPWQVSF NTTRKVMHYALKPVHSPMAGPIRAVAITVPLVVISAFATETTSCLLQNVSFGDYIIBLVDDF NTTRKVMHYALKPVHSPMAGPIRAVAITVPLVVISAFATETTSCLLQNVSFGDYIIBLVDDF NTTRKVMHYALLRERLERFRYFWFUCKSSKDGQMHWNVVQFCTAFTLQDPGCCEVALD LIMBDFSLCREGQREWVIQKIHESQPIIVVCSKGMKYFVDKKNYKHKGGRAGSGKGSLF LVANSALABKLRQNKQSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMDNLSSAL FPLCTFTTASRSRGMHTRQGREKELLPEQVRPVPIRRHLQHAPVY"
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Xiong, S., Zhao, Q., Rong, Z., Huang, G., Huang, Y., Chen, P., Zhang, S., Liu, L. and Chang, Z.
Liu, L. hibits PC-12 cell Differentiation by Interfering with Ras-Mitogen-activated Protein Kinase MAPK Signaling
J. Biol. Chem. 278 (50), 50273-50282 (2003)
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Direct Submission
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Homo sapiens interleukin 17 receptor-like protein long form
(ILL17RLM) mRNA, complete cds; alternatively spliced.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 127; DB 6; Length 4392;
Pred. No. 5.7e-16;
0; Mismatches 10; Indels
'note="unnamed protein product"
                                  /codon_start=1
/protein_id="CAD29034.1"
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/db_xref="taxon:9606"
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AF494208.1 GI:21667503
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Homo sapiens chromosome 3 clone RP11-157F20, complete sequence.
ACU97358
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SHLHSRDHGLOEPGQHTRQGSRRNYFRSKSGRSLYVAICNMHQPIDEEPDWFEKQFVP
FHPPPLRYREPVLEKFDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQH
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STDQTETSSLTESVSSSSGLGEEEPPALPSKLLSSGSCKADLGCRSYTDBLHAVAPL"
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note="contains a putative TIR domain and SH3 interaction
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
[ (bases 1 to 154606)
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Kaul,R.K., Olson,M.V., Raymond,C., Clendenning,J. and Haugen,E.D.
Direct Submission
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Box 352145, Seattle, WA 98195, USA
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Saenphimmachak, C., Phelps, K.A., Buckley, D., Raymond, C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Box 352145, Seattle, WA 98195, USA
3 (Dases 1 to 154606)
Kaul, R. K., Olson, W. V., James, R. A., Rouse, G., Wu, Z., Saenphimmachak, C., Phelps, K.A., Buckley, D., Raymond, C. and
                                                          domain; similar to sef; hIL-17RLM-L; alternatively
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Sequence Validation:
This sequence has been validated by Multiple Complete Digest
fingerprinting. Comparison of the experimentally derived digest
fragments with sequence-predicted fragments is given below.
The electronically-digested sequence consists of both insert and
vector, in order to accurately represent the entire circular BAC.
Small fragments below a variable cutoff (approximately 400-800 bp)
are not resolved in the fingerprint and hence do not appear
in the table. There are no significant remaining discrepancies
between the experimental and predicted values. Uniquely ordered
fragments are separated by dashed lines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an altermate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5'; RP11-263116 (UWGC:bc0327) AC092050, 123826-bp overlap 3'; RP11-241K3 (UWGC:bc0319) AC093928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BglII
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                                                                                                                                                                                    Sequencing vector: plasmid; L08752; 100% of rea
Chemistry: Dye-terminator ET; 96% of reads
Chemistry: Dye-terminator Big Dye; 4% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 154096 bases at least Q40
Consensus quality: 154548 bases at least Q30
Consensus quality: 154600 bases at least Q20
Web site: http://www.genome.washington.edu
Contact: wugchtgs@u.washington.edu
------- Project Information
Center project name: chr-3
                                                                                                                       Center clone name: RP11-157F20 (bc0274)
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exclude fragments <1.5kb.The Sfil-digested PCR product was cloned into distinct Drail sites of pME18S-FL3. Xhol sites just outside the Drail sites can be used to isolate the CDNA insert. Libraries were constructed by oligo-capping method. Custom primers used for sequencing (5' and primer [CTTCTGCTCTAAAAGCTGCG]; a' end primer [CTTCTGCTCTAAAAGCTGCG]; Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codoi gtart=1
/protein_id="CAC93798.1"
/brotein_id="CAC93798.1"
/db_xref="id1:15985.082"
/translation="MAPWLQLCSVFFTVNACLNGSQLAVAGGSGRAWGVDTCGWRGV
GPASRNSGLYNITPKYDNCTTYLNPVGRHVIADAQNITISQYACHDQVATIEWSPGA
LGIEFLKGFFVILEELKSEGRQCQQLILLKDPRKQLNSSFRRTGMESQPFLNMKFETDYF
VKVVPPPFSIKMSENTWERNYRPFFRTRACDLLLQPDNILACKPFWKPNNLNISQHGSDMQVSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /trānslation="mapwlqlcsvrftynacingsqlavaaggsgrargadtcgwrgv
gpasrnsglynitfkydncttylnpvckhviadaqnitisqyachdqvavtiiwspgv
letisqk"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATGGCCCCGTGGCTGCTCTCCGTCTTTTACGGTCAACGCCTGAACGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissue type="frontal lobe left"
/clone lib="macaque brain cDNA library QflA"
.dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="hypothetical protein"
/protein_id="BAC21616.1"
/db_xref="GI:24059742"
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/note="unnamed protein product"
                                                                                                                                                                                                                                                                                         1. .2037
/organism="Macaca fascicularis"
/mol_type="mRNA"
/db_xref="taxon:9541"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 125.4; DB 9 Pred. No. 1.3e-15;
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/mol type="unassigned DNA"
/db zref="taxon:9606"
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Sequence 1 from Patent WO0168859.
AX251723
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1. .3083
                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="Qf1A-18833"
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92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sex="male"
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EESSESSTYTAALPRERLRPRPKVFLCYSSKDGQNHWNVQCFAYFLQDFCGCEVALD
LWBDFSLCREGQREWYQKTRENQPTTTVCSKRGMENYPHGAGGGRGSGKGELF
LWAGSALAEKLRQARSALSKFTAVYPPYSCEGYPGILLDLSTYKTLMDNLPQLC
SHLHSRDHGLQBFGQHTRQGSRRNYFRSKSGRSLTVAICNMHQFIDEPDWFEKQFVP
FHPPPLKYREPVLEKPDGLALNDWNKCRPPEBEDFCLKKCHAPVTGATFGADSQHSGYH
GGLDQDGRARPALDGSALQPLIHTVKAGSSSBDMPRDSGIYDSSVPSSELSIFJMSGI
FTDQTFSSLTESVSSSGLGEEPPALPSKKLLSSGSCKADLGCRSYTDELHAVAP"
DHAPHNFGFR.FFYLHYKLKHEGPFKRKTCKQEQTTETTSCLLQNVSPGDY.I ELVDDT
NTTRKVWHYALKPVHSPWAGPIRAMAITVPLVVISAFATLFTVMCRKKQQENIYSHLD
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                                                                                                                                                                                                                                                                                                                                                                               Length 3083;
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                                                                                                                                                                                                                                                                                                                                                                                      DB 6;
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/note="unnamed protein product"
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Pred. No. 2.6e-15;
0; Mismatches 12
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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/product="unnamed"
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90.2%;
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ilarity 91.6%;
Conservative (
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AX350979
LOCUS
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VERSION
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TITLE
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SOURCE
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SOURCE ORGANISM

REFERENCE AUTHORS

DEFINITION

RESULT 11

BC066804

ACCESSION VERSION KEYWORDS 145

Matches

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Mus musculus strain BALB/c interleukin 17 receptor-like protein long form (Ill7rlm) mRNA, complete cds; alternatively spliced. AF494210
Series: IRAK Plate: 144 Row: e Column: 15
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 24025661.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xiong, 20., Huang, G.R., Zhao, Q.H., Chen, P.L., Rong, Z.L., Ye, X.Y., Chen, Y., Liu, L., Fu, X.Y. and Chang, Z.J.

Direct Submitseion

Submitted (22-MAR-2002) Tsinghua Institute of Genome Research,

Department of Biological Sciences and Biotechnology, and School of

Medicine, Tsinghua University, Beijing 100084, P.R. China

1. 2387
                                                                                                                                                                                                                                                                                                    /db xref="taxon:10090"
/clone="IMAGE:30091051"
/tissue_type="Neural Stem Cell, (Undifferentiated), adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone lib="NIA Mouse Neural Stem Cell (Undifferentiated) cDNA Library (Long)" /lab host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 2387)

Xiong, S., Zhao, Q., Rong, Z., Huang, G., Huang, Y., Chen, P., Zhang, S., Liu, L. and Chang, Z.

Hist Inhibits PC-12 cell Differentiation by Interfering with Ras-Mitogen-activated Protein Kinase MAPK Signaling
J. Biol. Chem. 278 (50), 50273-50282 (2003)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/note="type I receptor containing a putative TIR domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86 TCGCAGCTGGCAGTGGCCGCGGGCGGCTGCCGCGCGAGGGGCGCGGACACCTGTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75.6%; Score 112.6; DB 10; Length
86.7%; Pred. No. 4.8e-13;
tive 0; Mismatches 19; Indels
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                                                                                                                                                                                       /organism="Mus musculus"
/mol_type="mRNA"
/strain="CD1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pSPORT1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 TGGAGGATGAAAGCGGCTGCCCG 143
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/strain="BALB/c"
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Klausner, R. D., Collins, F. S., Wagner, L., Shenmen, C. M., Schuler, G. D.,
Altschul, S. P., Zeeberg, B., Buetow, K. H., Scheefer, C. F., Bhat, N. K.,
Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L.,
Scheetz, T. E., Brownstein, M. J., Usdin, T. B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S. S., Loquellano, N. A., Peters, G. J.,
Abramson, R. D., Mulley, S. J., Bosak, S. A., McEwan, P. J.,
Worley, K. C., Hale, S., Garcia, A.M., Gay, L. J., Hulyk, S. W.,
Villalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A.,
Sanchez, A., Whiting, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A. C., Shevchenko, Y.,
Bouffard, G. G., Blakesley, R. W., Touchman, J. W., Green, E. D.,
Buckson, M. C., Rodriguez, A. C., Grimwood, J., Schmutz, J., Myers, R. M.
Butterfield, Y. S., Krzywinski, M. I., Skalaka, U., Smailus, D. E.,
Schnerch, A., Schein, J. E., Jones, S. J. and Marra, M. A.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mod@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
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Tissue Procurement: Dr. Angelo L. Vescovi ( Institute fro Stem Cell
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2203)
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Submitted (01-WAR-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                   Gaps
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Mus musculus cDNA clone IMAGE:30091051, partial cds.
BC066804
        14; Indels
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Contact: MGC help desk
            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 121 TGGAGGATGAAAGCGGCTGCCCG 143
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                129; Conservative
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TITLE

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75.6%;
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IGIEFLKGFRVILEELKSEGROCQOLILKOPRQINSSFRRTRENESOPFLNWKFETDYF
VKIVPFPSIRONYHPF FRTRACDILLQPDNILACKPFWKFRNILNISQHGSDMHVSF
DHAPQNFGFRGFHVYALKHEGPFRRTRCDOQNTETTSCLLQNVSFGDYILELVDDS
NTTRKAAQYVKSVQSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQQRIYSHLD
ESPESSEYTAAALPRDRILROPRVFTCYSUKDGONHMVVYCCRAFLQDFGCGCVALD
LWEDFSLCREGQREWAIQKHESQFILVCSKGMKXFVDKWRFRHKGGSRGRAGEFC
LVAVAAIAEKURQAKQSSAALRKFIAVYFDYSCEGDVPCSLDLSTKYKLMDHLPFLC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HPPVRYQEPVLEKFDSGLVLNDVISKPGPESDFCRKVEACVLGAAGPADSYSYLESQH
VGLDQDTEAQPSCDSAPALQPLLHAVKAGSPSEMPRDSGIYDSSVPSSELSLPLMEGL
SPDQIETSSLTESVSSSGLGEEDPPTLPSKLLASGVSREHGCHSHTDELQALAPL"
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                                                                                                                                                                                      translation="MAPWLQLCSFFFTVNACLNGSQLAVAAGGSGRARGADTCGWRGV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="interleukin 17 receptor-like protein long form"
/protein id="AAM74079.1"
/db.xref="G1:21667508"
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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   interaction domain; similar to Sef;
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Pred. No. 4.7e-13;
0; Mismatches 19; Indels
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and a putative SH3 increases mIL-17RLM-L; alternatively spliced" /codon_start=1'...': 17 receptor-1
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/organism="Mus musculus"
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/db_xref="taxon:10090"
101. .2320
/note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA
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Sequence 11 from Patent WO0208259.
AX364580
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Location/Qualifiers
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Best Local Similarity 86.7%;
Matches 124; Conservative (
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VKI VPPPSIKNESWYTPPFFERTEXCHILLOPNILACKPFWKRRNLNISGHGSDMHVSF
DHAPQNFGFRGFHVLYKLKHEGPFRRTCRQDQNTETTSCLLQNVSPGDY I I ELVDDS
THTRRAAQYVXGSVQSWAGPTRAVATVTPLVYTSAPATLFTYMCRKKQQBNI YSHLD
BESPBSSTYAAALPPDRLRPQPKVFLCYSNROGQNHWNVQCFAYFLDDFGCCEVALD
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HPPVRYCBPVLIKFDSGLVAINVI SRCGPESDFCKKVBACVLGAAGPADSYSYLESQH
VGLDQDTEAQPSCDSAPALQFLLHAVKAGSFSEMPRDSGI YDSSVPSSELSLPLMEGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF459444 3366 bp mRNA linear ROD 15-MAY-2002
Mus musculus transmembrane protein (Sef) mRNA, complete cds.
AF459444
                      OHPPVRYQEPVLEKFOSGLVINDVISKPGPESDFCRKVEACVIGAAGPADSYSYLESQ
HVGLDQDTEAQPSCDSAPALQPLLHAVKAGSPSEMPRDSGIYDSSVPSSELSLPLMEG
LSPDQIETSSLTESVSSSGIGEEDPPTLPSKLFASGVSREHGCHSHTDELQALAPL"
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CAHLHSGEQEVLGQHPGHSSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFEKQFIPF
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Lin, W. and Ang, S.-L.
Direct Submission
Submitted (13-DEC-2001) I.G.B.M.C., 1, rue Laurent Fries, Illkirch
                                                                                                                                                                                                                                                                                                                                                                               120
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Mukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bummania; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3366)
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                                                                                                                                                                                                                                                                                                                                                                               161 TCGCAGCTGGCAGTGGCCGCGGGGCTCCGGCCGCGAAGGGGCGCGGACACCTGTGGC
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0
                                                                                                                                                           Length 2443;
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                                                                                                                                                           Score 112.6; DB 6;
Pred. No. 4.7e-13;
); Mismatches 19;
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63108, USA
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Unpublished (2001)
3 (bases 1 to 134122)
McPherson, J.D. and Waterston, R.H.
Direct Submitted (20-JUN-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
4 (bases 1 to 134122)
McPherson, J.D. and Waterston, R.H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (27-FEB-2003) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA (5 hases 1 to 134122) McPherson, J.D. and Waterston, R.H. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (08-MAY-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
6 (bases 1 to 134122)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap.
                                                                                                                                                                                                                                                 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 134122)
SPDQIETSSLTESVSSSGLGEEDPPTLPSKLLASGVSREHGCHSHTDELQALAPL"
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                                                                                                                                                                      23 ATGGCCCCGTGGCTGCTCTCTCTTCTTCTTCACTGTCAACGCCTGTCTAACGGC
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Mus musculus BAC clone RP24-366J2 from chromosome 14, complete
                                                                                                                                          1 ATGCCCCCTGCTGCTCTCCTCCTCTTTTACGGTCAACGCCTCAACGGC
                                                                                                    Gaps
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                                                           Length
                                                                                                    19; Indels
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The sequence of Mus musculus BAC clone RP24-366J2
Unpublished (2001)
2 (bases 1 to 134122)
                                                           DB 10;
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Contact: submissions@watson.wustl.edu
                                                       Score 112.6; DB 1
Pred. No. 4.5e-13;
0; Mismatches 19
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                                                                                                                                                                                                                                                                                                            121 TGGAGGATGAAAGCGGCTGCCCG 143
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Mus musculus
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AC125152.5 GI:30425598
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                                                           Query Match
Best Local Similarity 86.7%;
Matches 124; Conservative
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ORGANISM
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AUTHORS
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JOURNAL
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AC125152
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KEYWORDS
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                       ORIGIN
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between neighboring data submissions.
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu

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셤 ઠે SOURCE INFORMATION:
The RPCI-24 BAC Library has been constructed by Pieter de Jong and coworkers (http://www.chori.org) from male C57BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org

NEIGHBORING SEQUENCE INFORMATION

This sequence is the entire insert of the clone. This clone is overlapped by AC124603. Location/Qualifiers

FEATURES

1. .134122 Organism="Mus musculus" /mol_type="genomic DNA" /db_xref="taxon:10090" /chromosome="14" /clone_lib="RPCI-24"
312. .503
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repeat_region

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note="Likely pseudogene (HMM Sc=30.04 / Sec struct
cc=5.93).14161
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3621. .13690
product="tRNA-Ser"
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| /rpt_family="56 | /rpt_family="66 | /rpt_family="84" | /rpt_family="7494 | /rpt_family="74946 | 
                                                                                                                                             5368. 5449
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5548. 5574
/rpt_family="Alu"
5648. 5574
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6127. 6230
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7866. 7768
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Location/Qualifiers 86. .2347 /*tag= a /product= "Zcytor18" Gao Z; 23-JUL-2001; 2001WO-US023253 26-JUL-2000; 2000US-0220747P. Presnell SR, Kuestner RE, (ZYMO) ZYMOGENETICS INC. WPI; 2002-217048/27. P-PSDB; ABB07626. WO200208259-A2 31-JAN-2002.

New cytokine receptor polypeptide designatéd zcytor18, useful for inhibiting cell proliferation associated with psoriasis or tumor growth, and modulating immune system by binding to endogenous zcytor18 ligand.

Claim 5; Page 85-90; 119pp; English.

ADM94405 AAQ71197 AAA35296 AAF21418 ABZ97112

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ACA26238

The invention relates to an isolated cytokine receptor polypeptide

Disclosure; Page 94-98; 119pp; English.

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designated Zcytor18. The Zcytor18 polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with psoriasis or tumour growth. The encoding nucleic acids are useful for providing Zcytor18 in vivo by gene therapy techniques. Zcytor18 oligonucleotide probes are useful for in vivo diagnosis, and the Zcytor18 probes and primers can be used to detect and localize Zcytor18 gene expression in tissue samples. The probes are also useful for detecting gross aberrations in chromosome 3 in which Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in linkage-based testing of pulmonary alveolar proteinosis, familial periodic fever and erythroleukemia, and erythroleukemia associated with polymorphisms of cytokine receptors. The present sequence represents a human Zcytor18 nucleotide sequence
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                      The invention relates to an isolated cytokine receptor polypeptide designated Zcytor18. The Zcytor18 polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with psoriasis or tumour growth. The encoding mucleic acids are useful for providing Zcytor18 in vivo by gene therapy techniques. Zcytor18 oligonucleotide probes are useful for invivo diagnosis, and the Zcytor18 probes and primers can be used to detect and localize Zcytor18 gene expression in tissue samples. The probes are also useful for detecting gross aberrations in chromosome 3 in which Zcytor18 gene resides. The Zcytor18 polymucleotides can also be used in linkage-based testing of pulmonary alveolar proteinosis, familial periodic fever and erythroleukemia, and erythroleukemia associated with polymorphisms of cytokine receptors. The present sequence represents a human Zcytor18 variant nucleotide sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86 Argacccccraacracacrcracrccarcrrrrracarcaacaccraccaacac
inhibiting cell proliferation associated with psoriasis or tumor growl and modulating immune system by binding to endogenous zcytor18 ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGCTCCGTCTTTTACGGTCAACGCCTGCCTCAACGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2341;
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2341 BP; 550 A; 668 C; 625 G; 498 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cDNA encoding novel secreted protein LP253.
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 127; DB 6;
Pred. No. 2.1e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                                         Claim 5; Page 102-106; 119pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 TGGAGGATGAAAGCGGCTGCCCG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206 redadecedagrececedeceae 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABK62082 standard; cDNA; 4392
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19-OCT-2000; 2000US-0241779P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATGGCCCCCGTGGCTGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                            85.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                              93.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ELIL ) LILLY & CO
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-FEB-2002
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The invention relates to a novel human secreted polypeptide having sequence 90% identical to the polypeptide sequences of LP105, LP061, LP223, LP239(b), LP223(a), LP223(b), LP2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120
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                                                                                                                                                Novel polypeptides and polynucleotides of secreted proteins useful for treating various diseases such as multiple sclerosis, cancer, autoimmune diseases, osteoporosis, Alzheimer's disease and Parkinson's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 recenserrescrescrecrescrescresses and reconsecrescrescresses and reconsecrescresses and reconsecresses and reconsecresses and reconsecresses and reconsecresses and reconsecres and reconsecresses and reconsecresses and reconsecresses and reconsecresses and reconsecresses and reconsecret and reconsecresses and reconsecret and recons
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4392 BP; 1125 A; 1050 C; 1101 G; 1116 T; 0 U; 0 Other;
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Pred. No. 2.1e-21;
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                                                                                                                                                                                                                                                                                                                          Claim 1; Page 166-171; 235pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention describes novel nucleic acids encoding interleukin (IL) 17
receptor like polypeptides useful as vaccines and in gene therapy. These
receptor like polypeptides useful as vaccines and in gene therapy. These
conventions are according to the propertie of anti-alzheimer's, renal,
immunosuppressive, hepatic, anti-linglamatory, anti-alzheimer's, renal,
immunosuppressive, hepatic, anti-leukaenic, anti-infertility and
costeopathic, vascular, cytostatic, anti-leukaenic, anti-infertility and
coptibulations as a control of the nucleic acids and
coptibulation and the polypeptide (ILI) Tip) expression. These
controlling may be used to prevent and treat diseases associated with
controlling to example immune disorders (e.g. inflammation, diabetes and
controlling, for example immune disorders (e.g. inflammation, diabetes and
controlling disorders (e.g. anorexia, cacheria and septicaemia),
controlling disorders (e.g. anorexia, cacheria and septicaemia),
controlling disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
controlling disorders (e.g. osteoporosis, asthma and emphysema), skin disease
controlling disorders (e.g. osteoporosis, cancers (e.g. leukaemia, myeloma and
controlling and atherosclerosis, cancers (e.g. infertility and
controlling complements may also used as diagnostic probes to detect and
controlling and in the production of antibodies against the proteins and in
contigens in the production of antibodies against the proteins and in
controlling and antiagonists may also be used to down requiate
controlling and activity. This sequence encodes the human interleukin 17
controlling proteined and antiagonists may also be used to down requiate
controlling receptor like protein described in the method of the invention
controlling and activity. This sequence encodes the human interleukin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psoriasis and glaucoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                           /*tag= a
/product= "Interleukin 17 (IL-17) receptor like protein"
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ches 12;
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                                                                                                             'note= "No stop codon given"
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0; Mismatches
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Location/Qualifiers
                                                                                                                                                                                                                                                                                     16-MAR-2000; 2000US-0189816P.
28-NOV-2000; 2000US-00724460.
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Matches 131; Conservative
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                                                                                      'partial
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Key
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The invention relates to primate and rodent DNAX cytokine receptor subunit (DCRS) polypeptides and the polymucleotides encoding them. The receptors, or their portions may be useful as phosphate labelling enzymes to label general or specific substrates. The subunits may also be functional immunogens to elicit recognishing antibodies, or antigens be used as an immunogen for the production of antisera or antibodies capable of distinguishing between other cytokine receptor family members. A purified DCRS can also be used as a reagent to detect antibodies generated in response to the presence of elevated levels of expression, or immunological disorders which lead to antibody production to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide useful for detecting antibodies generated in response to presence of increased protein levels or immunological disorders.
                                                                                                                                                                                                                                                                                                                                       Human; DNAX cytokine receptor subunit 8; DCRS8; phosphate labelling; 88; gene therapy; protein therapy; immunological disorder.
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                                                                                                                                                                                                                                                                                         Human DNAX cytokine receptor subunit 8 (DCRS8) cDNA.
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Pred. No. 2.7e-20;
0; Mismatches 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 16; Page 21-25; 148pp; English.
142 regadegagagagagaccagccas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
70. .2286
                                                                                                                                   BP
                                                                                                                                AAS18134 standard; cDNA; 2786
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90.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                      AAS18134;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New cytokine receptor polypeptide designated zcytor18, useful for inhibiting cell proliferation associated with psoriasis or tumor growth, and modulating immune system by binding to endogenous zcytor18 ligand.
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                                                                                                                                                                                    Cytokine receptor; Zcytor18; cell proliferation; antipsoriatic; human; pulmonary alveolar proteinosis; familial periodic fever; antitumour; erythroleukemia; chromosome 3p14.3; gene therapy; mouse; ds.
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Pred. No. 6.1e-18;
0; Mismatches 19; Indels
                                                                                                                                                              Murine cytokine receptor, Zcytor18 nucleotide sequence.
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                                                                                                                                                                                                                                                                                           /*tag= a
/product= "mouse Zcytor18"
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TGGAGGATGAAAGCGGCTGCCCG 143
                      190 regandegardegeccaeccae 212
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                                                                                    ABA95037 standard; DNA; 2443 BP
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86.7%;
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Best Local Similarity 86.7
Matches 124; Conservative
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Pred. No. 5.2e-16;
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                                                               TGGAGGATGAAAGCGGCTGCCCG
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Best Local Similarity 59.74
Matches 89; Conservative
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31-JAN-2002.
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                                                                                                                                                                                                                              Human cytokine receptor, Zcytor18 degenerate coding sequence.
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es 34;
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                  121 TGGAGGATGAAAGCGGCTGCCCGACCCCG 149
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                                                                                                                                                                                          (first entry)
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P-PSDB; ABB07626.
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121
                                                                                                                                                         ABA95032;
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Matches
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The invention relates to an isolated cytokine receptor polypeptide designated Zcytor18. The Zcytor18 polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with psoriaais or tumour growth. The encoding nucleic acids are useful for providing Zcytor18 in vivo by gene therapy techniques. Zcytor18 oligonucleotide probes are useful for invivo diagnosis, and the Zcytor18 probes and primers can be used to detect and localize Zcytor18 gene expression in tissue samples. The probes are also useful for detecting gross aberrations in chromosome 3 in which Zcytor18 gene resides. The Zcytor18 polymocleotides can also be used in linkage-based testing of pulmonary alveolar proteinosis, familial periodic fever and erythroleukemia associated with polymorphisms of cytckine receptors. The present sequence represents a human Zcytor18 splice variant degenerate coding sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New cytokine receptor polypeptide designated zcytor18, useful for inhibiting cell proliferation associated with psoriasis or tumor growth, and modulating immune system by binding to endogenous zcytor18 ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytokine receptor; Zcytor18; cell proliferation; antipsoriatic; human; pulmonary alveolar proteinosis; familial periodic fever; antitumour; erythroleukemia; chromosome 3p14.3; gene therapy; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Zcytor18 splice variant degenerate coding sequence.
Disclosure; Page 109-110; 119pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-MAY-2002 (first entry)
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P-PSDB; ABB07628.
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Gorman DM;
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated cytokine receptor polypeptide designated Zcytor18. The Zcytor18 polypeptides can be expressed by catanated Zcytor18. The Zcytor18 polypeptides can be used to inhibit cell proliferation associated with psoriabis or tumour growth. The encoding nucleic acids are useful for providing Zcytor18 in vivo by gene charapy techniques. Zcytor18 eligonucleotide probes are useful for involved diagnosis, and the Zcytor18 probes and primers can be used to detect or vivo diagnosis, and the Zcytor18 probes and primers can be used to detect and localize Zcytor18 gene expression in tissue samples. The probes are and localize Zcytor18 gene expression in chromosome 3 in which zcytor18 gene resides. The Zcytor18 polymucleotides can also be used in linkage-based testing of pulmonary alveolar proteinosis, familial polymorphisms of cytokine receptors. The present sequence represents a murine Zcytor18 degenerate coding sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New cytokine receptor polypeptide designated zcytor18, useful for inhibiting cell proliferation associated with psoriasis or tumor growth, and modulating immune system by binding to endogenous zcytor18 ligand.
                                                                                                                                                                                                        Cytokine receptor; Zcytor18; cell proliferation; antipsoriatic; human; pulmonary alveolar proteinosis; familial periodic fever; antitumour; erythroleukemia; chromosome 3p14.3; gene therapy; mouse; ds.
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                                                                                                                                                                         Murine cytokine receptor, Zcytor18 degenerate coding sequence.
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                                                                    ABA95038 standard; DNA; 2217 BP.
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The invention relates to primate and rodent DNAX cytokine receptor subunit (DCRS) polypeptides and the polynucleotides encoding them receptors, or their portions may be useful as phosphate labelling enzymes to label general or specific substrates. The subunits may also be functional immunogens to elicit recognising antibodies, or antigens be used as an immunogen for the production of antisera or antibodies. A combination, e.g., including a DCRS can be used as an immunogen for the production of antisera or antibodies apable of distinguishing between other cytokine receptor family members. A purified DCRS can also be used as a reagent to detect antibodies generated in response to the presence of elevated levels of expression, or immunological disorders which lead to antibody production to the endogenous receptor. This sequence represents human DCRS8 reverse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide useful for detecting antibodies generated in response to presence of increased protein levels or immunological disorders.
                                                                                                                                                                                                                                                                Human; DNAX cytokine receptor subunit 8; DCRS8; phosphate labelling; ss; gene therapy; protein therapy; immunological disorder.
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                                                                                                                                                                                                        Human DCRS8 reverse translation generic cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 25-26; 148pp; English.
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AAS18135 standard; cDNA; 2214 BP.
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The invention describes an isolated, purified or enriched nucleic acid (1) comprising: any of 4 fully defined sequences (SEQ. ID NO: 1, 6, 17 and 14their coding regions; a nucleic acid having at least 75% sequence identity to a nucleic acid of (a); or complements of (a) or The methods and compositions of the present invention are useful for synthesising lipopeptides, particularly A54145 and NRRL 3143, exhibiting antimicrobial, antifungal or antiviral activity. This sequence represents the Streptomyces refuinces 024A (or NRRL 3143) biosynthetic locus.
antimicrobial; fungicide; virucide; gene therapy; lipopeptide synthesis; AS4145; NRRL 3143; antimicrobial; antifungal; antiviral; biosynthetic locus; 024A; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful for synthesizing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated, purified or enriched nucleic acid, useful for synthesizin
lipopeptides, particularly from the biosynthetic locus A54145 and NRRL
3143, that exhibits antimicrobial, antifungal or antiviral activity.
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55.6%; Pred. No. 0.95
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                               Zazopoulos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prokaryotic essential gene #7895.
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                                                                                                                                                                                                                                                                                                                                                                                 (ECOP-) ECOPIA BIOSCIENCES INC
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17-APR-2002; 2002US-0372789P.
03-SEP-2002; 2002US-00232370.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACA26238 standard; DNA; 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-JUN-2003 (first entry)
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                                                                                                 Streptomyces refuineus
                                                                                                                                                                                                                                                                                                                                                                                                                               Staffa A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-852784/79.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                             US2003198981-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80;
                                                                                                                                                                                            23-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                               Farnet CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes an isolated, purified or enriched nucleic acid (I) comprising; any of 4 fully defined sequences (SEQ. ID NO: 1, 6, 17 and 34), and their coding regions; a nucleic acid having at least 75% sequence identity to a nucleic acid of (a); or complements of (a) or The methods and compositions of the present invention are useful for Synthesising lipopeptides, particularly A54145 and NRLL 3143; exhibiting antimicrobial, antifungal or antiviral activity. This sequence represents ORF4 of the Streptomyces refuineus 024A (or NRRL 3143) biosynthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated, purified or enriched nucleic acid, useful for synthesizing lipopeptides, particularly from the biosynthetic locus A54145 and NRRL 3143, that exhibits antimicrobial, antifungal or antiviral activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                       antimicrobial; fungicide; virucide; gene therapy; lipopeptide synthesis;
A54145; NRRL 3143; antimicrobial; antifungal; antiviral;
biosynthetic locus; 024A; ORF4; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2636 ridecechececeriderencerececedenacececedeseancecenecerecen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18876 BP; 2128 A; 7584 C; 7023 G; 2141 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 18876;
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llarity 55.6%; Pred. No. 0.89;
Conservative 0; Mismatches 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptomyces refuineus 024A locus (NRRL 3143).
                                                                           Streptomyces refuineus 024A locus ORF4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 4; SEQ ID NO 42; 69pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2756 GGCGGAGGCTGATCGCCGCCCGGC 2779
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17-APR-2002; 2002US-0372789P.
03-SEP-2002; 2002US-00232370.
                                                                                                                                                                                                                                                                                                                                                           24-DEC-2002; 2002US-00329079
                             (first entry)
                                                                                                                                                                                                                  Streptomyces refuineus
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ses 80; Conserv
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                             22-APR-2004
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21-MAR-2002; 2002WO-US009107. 21-MAR-2001; 2001US-00815242

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The invention relates to an isolated mucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding cantisense nucleic acid; (4) an antibody capable of specifically binding confideration or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway or the proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, a activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent of the which each of the strains is present in a culture or collection of strains; or (13) identifying the carget of a compound that inhibits the contribution of an organism. The antigens encoles acids are useful for proliferation of an organism. The antigense nucleic acids are useful for the proliferation of an organism. The engence or encoles of the arget of a compound collection of an organism. The antigense nucleic acids are useful for the proliferation of an organism. The antigense nucleic acids are useful for the proliferation of an organism. The antigense nucleic acids are useful for the proliferation of an organism and the control or and organism and antigense a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. acruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78 CGCTGGCGGGTCCGGCCGCGCGCGGCCGACACCTGTGGCTGGAGGATGAAAGCGGC 137
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Xu HH;
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25.8%; Score 38.4; DB 8; Length 567;
Best Local Similarity 57.5%; Pred. No. 4.4;
Matches 69; Conservative 0; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                  Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 567 BP; 72 A; 219 C; 195 G; 81 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                     Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 14; SEQ ID NO 14108; 1766pp; English.
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Carr GJ,
                                                                                                                          06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                  (ELIT-) ELITRA PHARM INC.
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Trawick JD,
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                                                                                                                                                                                                                                                                                                                        Wang L,
Wall D,
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ORGANISM: Human
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Sequence 1773, Ap
Sequence 1273, Ap
Sequence 14112, A
Sequence 1645, Ap
Sequence 1528, Ap
Sequence 1143, Ap
Sequence 1143, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4834, Ap Sequence 5926, Ap Sequence 5911, Ap Sequence 5979, Ap Sequence 1219, Ap Sequence 6342, Ap Sequence 6342, Ap
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452, App
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Sequence 3811, i
Sequence 3651, i
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Sequence 1
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(c) 1993 - 2005 Compugen Ltd.
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US-09-952-991A-14341

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Sequence 5805, Application US/09949016
; Sequence 5805, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
    APPLICANT: VENTER, J. Craig et al.
    TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: 05/241,755
; CURRENT FILING DATE: 2000-04-14
; PRIOR RILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; TEMPARE: PastSEQ for Windows Version 4.0
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US-09-949-016-17547/c
; Sequence 17547, Application US/09949016
; Sequence 17543
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENYER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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Sequence 2, Appli
Sequence 1, Appli
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Sequence 2026, A
Sequence 255, Ap
Sequence 4081, A
Sequence 4108, A
                                                                                                          Sequence 907, Ap
Sequence 8481, A
Sequence 1128, A
Sequence 952, Ap
Sequence 8394, A
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Pred. No. 1.1;
0; Mismatches 60; Indel8
US-09-902-540-4306
US-09-252-991A-3607
US-09-902-540-1214
US-09-252-991A-907
US-09-252-991A-918
US-09-252-991A-1128
US-09-252-991A-912
US-09-252-991A-8134
US-09-252-991A-8147
US-09-252-991A-8147
US-09-902-540-768
US-09-103-840A-1
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US-09-640-211A-2026
US-09-640-211A-255
US-09-255-991A-4081
US-09-252-991A-4108
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Best Local Similarity
Matches 85; Conserv
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us-10-717-282-1_copy_86_234.rni

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ORGANISM: Human
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APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Wyxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT APPLICATION NUMBER: 05/17/10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
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                                                                                                                                                                                                                                                                                                                                                                                                                          Score 38; DB 4; Length 84870;
Pred. No. 1.5;
0; Mismatches 60; Indels
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; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1273
          CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 17547
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                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: misc_feature
; LOCATION: (1)...(84870)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17547
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 25.5%;
Best Local Similarity 58.2%;
Matches 85; Conservative
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APPLICANT: Goldman, Barry S.
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SEQ ID NO 1273
FILE REFERENCE: CL001307
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NAME/KEY: unsure
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ORGANISM: Human
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ABELICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PAPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRASESEQ for Windows Version 4.0
LENGTH: 50109
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERGIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER: OS 60/094,190
RIOR FILING DATE: 1998-07-27
NUMBER: OS 60/094,190
RIOR FILING DATE: 1998-07-27
NUMBER: OS 60/094,190
ERIOR FILING DATE: 1998-07-27
NUMBER: OS 60/094,190
ERIOR FILING DATE: 1998-07-27
NUMBER: OS 60/094,190
24788 CAGGGGCTCCGCCTCCATGCCCAGCGCCGCGGCGAAGGCGGCGGCGGCCGCCGCCGC
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Pred. No. 3.1;
0; Mismatches
                                                                                                                                                                                                                                                                                                     Sequence 14112, Application US/09949016 Patent No. 6812339
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Patent No. 6551795
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 60.6%;
Matches 60; Conservative
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Sequence 8317, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: US 0/074,788

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR PRILING DATE: 1998-02-18

PRIOR FILLING DATE: 1998-02-18

PRIOR PILLING DATE: 1998-07-27

SEQ ID NO 8317
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                                                                                       320 AAGACGCCCGCCCAGGCCCCTCCACGGCGCGCGGCGAGGCCAGGCCACCTCCACCGGGAAG 261
APPLICANT: Hinche, Green C.
APPLICANT: Hinche, Green C.
APPLICANT: Slater, Steven C.
APPLICANT: Riegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849) B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1143
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23.1%; Score 34.4; DB 4; Length 19598;
Best Local Similarity 52.9%; Pred. No. 10;
Matches 74; Conservative 0; Mismatches 66; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: unsure

| LOCATION: (1)..(19598)

| OTHER INCRMATION: unsure at all n locations

US-05-902-540-1143
                                                                                                                                                                                                                                                                                                                                          Sequence 1143, Application US/09902540; Patent No. 6833447; GENERAL INFORMATION: APPLICANT: Goldman, Barry S.
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US-09-252-991A-8317/c
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US-09-902-540-1143
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US-09-22-991A-1528/c
US-09-22-991A-1528, Application US/09252991A

Sequence 1528, Application US/09252991A

Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: ALENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Slater, Steven C.

APPLICANT: Slater, Steven C.

TITE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: 08/09/902,540

CURRENT FILING DATE: 2001-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 3148

LENGTH: 1437
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Pred. No. 8.5;
0; Mismatches 66; Indels 0
                            Indels
                            29;
    64.6%; Pred. No. 4.3;
                            0; Mismatches
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Best Local Similarity 52.9%;
Matches 74; Conservative (
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       Local Similarity 64.69
nes 53; Conservative
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US-09-902-540-3148/c
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                                                                                              Score 34.2; DB 4; Length 1167;
Pred. No. 9.4;
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APPLICANT: HUTCHINSON, Charles R.
APPLICANT: HUTCHINSON, Charles R.
APPLICANT: FILIPPINI, SILvia
TITLE OF INVENTION: PROCESS FOR PREPARING DAUNORUBICIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STAIL:
COUNTRY: USA
ZIP: 2005-5701

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNDERR: US/08/660,765A
FILING DATE: 10-UNN-1996

""ACSTRICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATGGCCCCGTGCTGCTGCTCTCCGTCTTCTTTACGG
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Pred. No. 9.5;
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ATTORNEY/AGENT INFORMATION:
NAME: BERMAN, RICHARD J. RECISTRATION NUMBER: 39,107
REFERENCE/DOCKET NUMBER: P1615
TELECOMMUNICATION INFORMATION:
TELEFAX: 202/638-5000
TELEFAX: 202/638-6100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                   23.0%;
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     US-09-252-991A-14278
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US-09-252-991A-14341/C
US-09-252-991A-14341/C
Sequence 14341, Application US/09252991A
Sequence 14341, Application US/09252991A
Sequence 14341, Application US/09252991A
FAPLICANT: Marc J. Rubenfield et al.
GENERAL INFORMATION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILLE REPERENCE: 107196.136
FILLE REPERENCE: 107196.136
CURRENT FILLING DATE: 1999-02-18
FRIOR FILLING DATE: 1998-02-18
FRIOR PRIOR PRILING DATE: 1998-02-18
FRIOR FILLING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 14341
LENGTH: 1092
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Sequence 14278, Application US/09252991A

Fatent No. 6551795

Fatent No. 6551795

FATENT No. 6551795

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT PALLIA DATE: 1999-02-18

PRIOR PLING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 14278

LENGTH: 1167
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                                                                                                                                                                                                                                                                                                                                                                        53; Indels
                                                                                                                                                                                                                                                         Score 34.2; DB 4;
Pred. No. 8.9;
0; Mismatches 53;
; LENGTH: 531
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8317
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ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity 55.5%;
Matches 66; Conservative
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Best Local Similarity 55.5
Matches 66; Conservative
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NAME/KEY: unsure
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US-09-902-540-6461
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PLING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 14673
LENGTH: 102406
                                        ABELICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE REPERBENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRASESEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 12388
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23.0%; Score 34.2; DB
Best Local Similarity 56.8%; Pred. No. 13;
Matches 63; Conservative 0; Mismatches
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    Sequence 12388, Application US/09949016
Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LUCATION: (1)...(94156)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12388
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OTHER INFORMATION: n = A,T,C or
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Best Local Similarity 56.8
Matches 63; Conservative
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NAME/KEY: misc_feature
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LOCATION: (1)...(94156)
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APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Rooter C.
TITLE OF INVENTION: Wyxococcus xanthus Genome Sequences and Uses Thereof FILE REPRENCE: 38-10(15849) B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR PILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 6461
GGTCAACGCCTGCCTCAACGGCTCGCAGCTGTGGCCGCTGGCCGCTGGCGGGTCCGGCCGCGC
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COTHER INFORMATION: unsure at all n locations
US-09-902-540-6461
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                                                                                                                                                                                                                                                                                                 Sequence 6461, Application US/09902540 Patent No. 6833447 GENERAL INFORMATION: APPLICANT: Goldman, Barry S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.7%;
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Matches 59; Conservative
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AL829621 OGWDB22TH AJ679503 SCJLR2102

CN412351 BU51869388 BU51869388 BEF83051 CL507788 AZ047386 AZ047386 AL679501 CC660832 CC774305 CC774305 CC774305 CC774305 CC774375 CR33161 CC673305 CC77778 AU177782 AU177782 BU970198 BU970198

603254956

AGENCOURT 601470628

OR_CBa000 OR_BBa008 602612565

FGAS02506 AV939902 HB13018r

AU177782

Sequence:

Run on:

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Contact: Robert Strausberg, Ph.D.

Email: Gapbs-r@mail.nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento
Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The

I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
infocimage.llnl.gov
infocimage.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 492.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nae01a12.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3434014 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I bases 1 to 585; NCT-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCT-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
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/organism="Homo sapiens"
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Location/Qualifiers
CN412342
CN412351
CN412352
BG718697
BU509388
BE783051
CL507788
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BIS62240
AL829621
CCG66083
AJ679503
CA149067
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AV939902
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Homo sapiens
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Unpublished (1997)
                                   710
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KEYWORDS
SOURCE
ORGANISM
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TITLE
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CF260435
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                     version 5.1.6
- 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                              OM nucleic - nucleic search, using sw model
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149
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CN412349
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Gapop 10.0 , Gapext 1.0
                       GenCore (c) 1993 .
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Maximum DB seq length: 200000000
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gb_est2:*;
gb_est3:*
gb_est4:*;
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gb_gs81:*;
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38.8
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Database

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ORIGIN

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1217928-1220615); NCI CGAP_CO10 pool 1 LLAM 2644-2653, 2871-2872 (IMAGE CloneIDS 1057416-1061255,1144584-1145351). (6% of the driver population), plus a pool of 3, 440 arrayed clones from NCI CGAP_Sub1 (IMAGE CloneIDS 2708616-2710535) and NCI_CGAP_Sub2 (IMAGE CloneIDS 2708616-2710535) and the driver population), plus a pool of 11,136 clones from NCI CGAP_Sub3 (IMAGE CloneIDS 2712456-272359) (10% of the driver population), plus a pool of 5,472 clones from NCI CGAP_Sub4 (IMAGE CloneIDS 2723522-2729326) (40% of the driver population), plus a pool of 4032 clones from NCI CGAP_Sub6 (IMAGE CloneIDS 2728969-2733190) (40% of the driver population). Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches 10 Pacilitate Gene Discovery. Genome Research 6, 791-806. TAG_SEQ=None found"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            K0971D08-5N NIA Mouse Neural Stem Cell (Undifferentiated) CDNA Library (Long) Mus musculus cDNA clone NIA:K0971D08 IMAGE:30091051 5, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
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/db_xref="taxon:10090"
/clone="NIA:K0971D08 IMAGE:30091051"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .474
/organism="Mus musculus"
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/strain="CD1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CA879041.1 GI:27330590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 131; Conservative
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Best Local Similarity
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KEYWORDS
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CA879041
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// (Johne="Induce: 1000")
// (Johne="Induce: 1000")
// (Johne="Induce: 1000")
// (Johne="Vector: pir730-Pac (Pharmacia) with a modified
ja a butracted library had ill most performed from NCI CGAP Subb (The
// (Johne Pac Induce Indu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: NCI-CGAP clone distribution
information can be found through the I.M.A.G.B. Consortium/LLML at:
www-bio.llnl.gov/bbrp/image.html The following repetitive
elements were found in this cDNA sequence: 24-56,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST 07-DEC-2000
                                                                                                                                                                                                                 90 ATGGCCCCGTGCCTGCAGCTCTGCTCTTTTACGGTCAACGCCTCAACGGC 149
                                                                                                                                                                                                                                                                                          9
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1 (bases 1 to 230)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NATIONAL Gancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               230 bp mRNA linear EST 07-DEC-:
UI-H-BW1-anq-g-12-0-UI.s1 NCI CGAP_Sub7 Homo sapiens cDNA clone
BF515598
                                                                                                                                                                                     Gaps
                                                                                                                                  .;
0
                                                                      Length 585;
                                                                                                                               Indels
                                                                         Score 126.8; DB 4;
Pred. No. 2.8e-21;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .230
/organism="Homo sapiens"
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/db_xref="taxon:9606"
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Seg_primer: M13 Forward
POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BF515598.1 GI:11600777
                                                                         Query Match
Best Local Similarity 98.5%;
Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
Homo sapiens
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TITLE
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BF515598
LOCUS
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KEYWORDS
SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. E. (bases 1 to 665)

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y. RIEN Mouse ESTS (Arakawa, T., et al. 2001)

L. Unpublished (2001)

Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sall/NotI site of pSPORTI plasmid vector. The DH10B B. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 3.8 kb. The library was constructed by Yulan Piao."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST 26-OCT-2001
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Tel: 81-45-503-9222
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lib="NIA Mouse Neural Stem Cell (Undifferentiated)
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BB641245 BIKEN full-length enriched, 10 days neonate cortex Mus musculus cDNA clone A830013G13 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 112.6; DB 6;
Pred. No. 9.1e-18;
0; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 récadegeagradedecedecad 168
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BB641245.1 GI:16476370
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86.7%;
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Best Local Similarity 86.7
Matches 124; Conservative
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ORGANISM
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VERSION
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JOURNAL
COMMENT
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BB641245
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Authorizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Alzawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Alzawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K.
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Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Inch,M., Komno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Tonoue,K., Togava,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
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/dev_stage="10 days neonate"
/lab_host="DH108"
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86.7%; Pred. No. 9.1e
ive 0; Mismatches
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/db_xref="taxon:10090"
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Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Rokazeki, Y., Futuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yaqi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Kiyosawa, H., Yaqi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Kiyosawa, H., Yaqi, K., Saito, R., Maraelli, R., Matain, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C.F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,
                                                                                                                                                                                                                                                                                                                                                                                   Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY152713 RIKEN full-length enriched, B16 F10Y cells Mus musculus cDNA clone G370032A13 5', mRNA sequence.
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Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tismue_type="pooled"
/lab_host="DH1DB"
/clone_tib="MARC 4BOV"
/note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sal1;
Library made from pooled tissue From day 20 and day 40 embryos."
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                                                                                                                                                                                                                                                        USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
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BACKWARD: GTTTTCCCAGTCACGACG
Plate: 112 row: C column: 10
Seg primer: ATTTAGGTGACACTATAG
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Contact: Smith TPL
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Fax: 402 762 4390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://baygenomics.ucsf.edu/
http://baygenomics.ucsf.edu/
Unpublished (2001)
Contact: BayGenomics
Bay Area Functional Genomics Consortium (BayGenomics)
Bayi Area Functional Genomics Consortium (BayGenomics)
Bail: info@baygenomics.ucsf.edu
Bequence tag generated by 5' RACE of total RNA from gene trap ES
Cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from BayGenomics. Annotation
information available from
http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=
CELL_LINE&EX=XST163
                                                                                     CCI78870 239 bp mRNA linear GSS 02-MAY-2003
XST163 BayGenomics Gene Trap Library pGT1TMpfs Mus musculus CDNA,
mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOLINGS, D.C.

1 (base 1 to 547)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C.,
Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 TCGCAGCTGGCAGTGGCCGCGGGCGGCTCCGGCCGCGAGGGGGCGCGGGACACCTGTGGC 233
                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 239)
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATGGCCCCGTGCCTCTGCTCCGTCTTTTACGGTCAACGCTGAACGCTCAACGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="Male"
| cell_type="Embryonic stem cell"
|/clone|il="BayGenomics Gene Trap Library pGT1TMpfs"
|/note="Vector: pGT1TMpfs"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/mol_type="mRNA"
/strain="129 ola"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Class: Gene Trap.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
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CC178870.1 GI:30317421
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Matches 117; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus
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VERSION
KEYWORDS
SOURCE
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AUTHORS
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JOURNAL
COMMENT
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CC178870
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KEYWORDS
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BE750478
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27; Indels

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Vector sequences were eliminated by RepeatMasker version 2002/07/13 and crossmatch version 0.990319
Low quality bases were trimmed based on the quality values.
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/clone_lib="full-length enriched swine cDNA library, adult
ovary"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP154750 tull-length enriched swine cDNA library, adult ovary Sus scrofa cDNA clone OVRM10115H10 5', mRNA sequence.
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Ueniabit,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H.,
Uchumra,N., Hamasima,N. and Awata,T.
PEDB (Pig EST Data Explorer): construction of a database for ESTs
derived from porcine full-length cDNA libraries
Nucleic Acids Res. 32 (1), D484-D488 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 TOGCAGCTTGGCTGTTGGCCGCGTCCGGCCGCGCGCGGGGCGCCCGACACTGTGGC 120
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38 Aresceccerestracascreterrerererreresecercasceceresece
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Animal Genome Laboratory, Genome Research Department
National Institute of Agrobiological Sciences
2 Ixenodai, Tsukuba, Ibaraki 305-8602, Japan
Tel: +81-29-838-8627
Fax: +81-29-838-8627
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0; Mismatches 27; Indels
                                 0; Mismatches
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/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="OVRM10115H10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGAGGATGAAAGCGGCTGCCCGAC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        225 recadeseas receseces 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP154750
BP154750.1 GI:40404223
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                                      Matches 118; Conservative
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Best Local Similarity
Matches 116; Conserv
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SOURCE
ORGANISM
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Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
Numata,K., Oxido,T., Pavan,W.J., Pertea,G., Pesole,G.,
Petrovsky,N., Pillai,R., Pontius,Ju.O., Oi,D., Ramachandran,S.,
Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
Verardo,R., Wagner,L., Wallestedt,C., Wang,Y., Watanabe,Y.,
Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanaglsawa,M., Yang,I.,
Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
Hayatsu,M., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
Arakawa,T., Pukuda,S., Hara,A., Hashizume,W., Imotani,R., Inotani,R.,
Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
Raplysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNas
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Alzawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Hirozante, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
Hayashizaki, Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Computational Analysis of Full-Length Mouse cDNAs Computational Analysis of Full-Length Mouse CDNAs to
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequence din Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Broyclopedia Project of Genome Research in Riken contributed to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MSC 4472 Bethesda, Maryland U.S.A) whose assistance we gratefully
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/organism="Mus musculus"
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/clone="G370032A13"
/cell_type="B16 F10Y cells"
/clone_lib="RIKEN full-length enriched, B16 F10Y cells"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Yoshihide Hayashizaki
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MEDLINE PUBMED COMMENT JOURNAL

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97

121 TGGAGGATGAAAGCGGCTGCCCG 143

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Length 483;

Score 101.8; DB 5; Pred. No. 4.3e-15;

68.3%; 81.4%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     German Genetrap Consortium (GGTC)

Email: info@genetrap.de
UJCEO gene trap. Sequence tag generated by 5'RACE. Additional
sequence information can be found at:
http://genetrap.gsf.de/project/web_new/database/result_clone.html?
clone_id=G049F09' ES cell line harboring insertion mutation of
target gene is available at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.htm
1. Inhouse Sequence Identifier: 16755
Class: Gene Trap.
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AL450535.1 GI:11601943
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                                                                                                                CL212737 134 bp mRNA linear GSS 30-JUN-2004 G049F09 GGTC Gene Trap Library GV07C05 Mus musculus cDNA clone
                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 134)
Hansen,J., Floss,T., van Sloun,P., Fuchtbauer,E.M., Vauti,F., Arnold,H.H., Schnutgen,F., Wurst,W., Von Melchner,H. and Ruiz,P. A large-scale, gene-driven mutagenesis approach for the functional analyais of the mouse genome Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)
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Hordeum vulgare subsp. vulgare
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
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/cell type="Embryonic stem cell"
/cell_line="esc cells [CS7BL/6J x 12986/SvEvTac] Fl"
/clone lia="GGC Gene Trap Library GV07CO5"
/note="Vector: U3CEO"
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34.6%; Score 51.6; DB 9; Length 134;
Best Local Similarity 70.3%; Pred. No. 0.012;
Matches 83; Conservative 0; Mismatches 34; Indels
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/organism="Mus musculus"
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/clone="G049F09"
|||||||
158 TGGAGGGAGTGGGCCGGCCAG 180
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/strain="129 Sv"
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                                                                                                                                          G049F09, mRNA sequence.
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/clone lib-"Hotocoum vulgare Barke etiolated leaves"
/clone lib-"Hotocoum vulgare SK-; Site_1: Sal1; Site_2:
/note="Vector: pBluescript SK-; Site_1: Sal1; Site_2:
/note; mRNA was made from etiolated leaves of spring barley
variety 'Barke', a high quality malting variety. Plants
were grown on filterpaper for 6 d at 25 C in the dark.
Leaves were harvested at daylight conditions. Sal-Adaptor
Sequence: TCGACCACGGCGC Average insert size is 1 kb
Sequence trimming: Vector sequences and sequence ends were
trimmed from the 5'-and 3'-end until a 50 bp window
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EBro04_SQ003_H20_R root, 3 week, salt-stressed, cv Optic, EBro04
Hordeum vulgare gubsp. vulgare cDNA clone EBro04_SQ003_H20 5', mRNA
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.

1 (Bases I tro 271)

1 (Bases I to 271)

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2 (Contact: Metalek, W., Pleissner, K.-P. and Graner, A.

2 (Contact: Michalek W

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Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae;
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1 (bases 1 to 573)
Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardle, L., Ramsay, L., Machray, G., Marshall, D. F.M. and Waugh, R.
Development of Barley Transcriptome Resources
Unpublished (2001)
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/tissue_type="etiolated leaves"
/lab_host="XL1Blue"
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Invergowite, Dundee, DD2 5DA, Scotland,
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
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Genome Dynamics/Computational Biology
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/cultivar="barke"
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                                                                                                                                                                                                                                                                                                   /clone lib="root, 3 week, salt-stressed, cv Optic, EBro04" /note="Vector: pSPORT1; Site_1: Sal I; Site_2: Not I; Non-normalised library, directionally cloned into pSPORT1. Derived from roots of 3 week old salt stressed barley plants. Developed as part of the barley transcriptome resources of BBSRC/SEBRAD funded cereal IGF (Investigating
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (bases 1 to 854)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D.,
Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W.,
Fenton,R.D., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource
for barley genomics: Morex drought-stressed seedling shoot cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 GGCCCGCGGCGGGGGGCCCCCTCGCCGTCGCCCCACCGCCGGCGTCTCCGGCCC 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2001)
On Dec 19, 2000 this sequence version replaced gi:11895090.
Contact: Wing RA
Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
Email: est@scri.sari.ac.uk
All sequence has a Phred quality score of 20 or over
Seg primer: M13 reverse.
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/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28.9%; Score 43; DB 4; Length 573; 60.9%; Pred. No. 1.5;
                                                                                                             organism="Hordeum vulgare subsp. vulgare"
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Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                           /mol type="mRNA"
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/sub species="vulgare"
/db xref="teaxon:112509"
/clone="EBro04_S0003_H20"
/tissue type="root"
/dev stage="3 week"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 1.5;
0; Mismatches
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Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 526.
Location/Qualiflers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BF630932.2 GI:13091792
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Matches 70; Conservative
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with water, nystatin and cefotaxime in covered crystallization dishes. Five-day old seedlings were incubated at 90% RH for 24 hr. Shoots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, 600000 pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids. These steps were performed in the TJ Close laboratory at the University of California, Riverside (Choi, Close,
                                                                                                                                                                                                                                                                HVCDNAQ002 (Dehydration stress) ". hote="Vector: lambdaZAP, Site_1: EcoR1; Site_2: Xho1; Ance="Vector: lambdaZAP, Site_1: EcoR1; Site_2: Xho1; Seeds were surface startlized then germinated under axenic conditions in the dark at room temperature on filter paper
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pencion). Phagemids were plated and picked at the Clean University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
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/clone="HVSWEb0014Hlf"
frismue type="Seedling shoot"
11ab host="TUC121"
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Sarcocystidae; Neospora.
1 (bases 1 to 513)
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Neospora caninum
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/clone lib="Nc-1 Tachyzoite cDNA Library 2"
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XhoI; The cDNA library was constructed by Kellang Tang,
and Robert Cole at Washington University. CDNA was
synthesized from poly mRNA using an oligo-dr primer
containing a XhoI site. Following second strand synthesis,
EcoRI adapters were ligated to the CDNA, and products were
size-selected on sephacryl S500. The cDNA were
directionally cloned into the EcoRI/KhoI prepared
pBluescript II SK+ vector, and electroporated into GCI0
Competent Cells(PGC). The library may contain a small
percentage of host or bacterial contaminants."
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Contact David Sibley (toxoest@borcim.wustl.edu) for further
information relating to organism, libraries, or clone availability.
Seg primer: T3.
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USDA-WashU Neospora EST Project
Washington University School of Medicine
4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
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Sarcocystidae; Neospora.
1 (bases 1 to 598)
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/lab_host="ElectroTen Blue cells (Stratagene)"
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                                                                            /organism="Neospora caninum"
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  Seq primer: -40RP from Gibco.
Location/Qualifiers
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Neospora caninum
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Matches 61; Conserv
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/clone lib="Nor-Inv Tachyzoite CDNA Library"
/note="Vector: pBluescript II SK+Vector type: plasmid;
Site 1: EcoRI; Site 2: XhoI; The cDNA library was
constructed by Keliang Tang, and Robert Cole at Washington University. cDNA was synthesized from Poly(A) + mRNA using an oligo-d(T) primer containing a XhoI site. Following second strand synthesis, EcoRI adapters were ligated to the CDNA, and products were size-selected on sephacryl S500. The cDNA were directionally cloned into the EcoRI/XhoI prepared pBluescript II SK+ vector, and electroperated into ElectroTen Blue cells (Stratagene).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryotta, Alveolata, Apicomplexa, Coccidia, Eimeriida, Sarcocystidae, Neospora.

1 (bases 1 to 565)
Cole, R., Fogarty, S., Tang, K., Howe, D.K., Sibley, L.D., Clifton, S., Marra, M., Hillier, L., Pape, D., Martin, J., Wylie, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennet, J., Ronko, I., Tsagareishvii, R., Fedele, M., Belaygorod, L., Franklin, C., and Wilson, R. Wagnire, L., Wadkins, J., Richey, J., Waterston, R. USDA-MashU Neospora EST Project
                                                                                                         Contact David Sibley (toxoest@borcim.wustl.edu) for further information relating to organism, libraries, or clone availability. Seq primer: T3
High quality sequence stop: 509.
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Contact David Sibley (toxoest@borcim.wustl.edu) for further
information relating to organism, libraries, or clone availability.
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USDA-WashU Neospora EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Park Parkway, Box 8501, St. Louis, MO 63108, USA
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                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:29176"
                                                                                  est@watson.wustl.edu
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Tel: 314 286 1800
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ORIGIN

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Gaps

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/clone lib="Nc-LIV Tachyzoite cDNA Library"
/note="Vector: pBluescript II SK+Vector type: plasmid;
Site 1: BcoRI, Site 2: Xho!; The cDNA Hibrary was
constructed by Keliang Tang, and Robert Cole at Washington
University. CDNA was synthesized from Poly(A) + mRNA using
an oligo-d(T) primer containing a XhoI site. Following
second strand synthesis, EcoRI adapters were ligated to
the cDNA, and products were size-selected on sephacryl
SSOO. The CDNA were directionally cloned into the
ECORI/XhoI prepared pBluescript II SK+ vector, and
electroporated into ElectroTen Blue cells (Stratagene).
The library may contain a small percentage of host or
bacterial contaminants."
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ORIGIN

Query Match 28.1%; Score 41.8; DB 7; Length 598; Best Local Similarity 65.6%; Pred. No. 2.9; Matches 61; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

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Search completed: August 16, 2005, 05:21:56 Job time : 3183 secs

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August 9, 2005, 11:33:31; Search time 121.831 Seconds (without alignments) 2390.439 Million cell updates/sec
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1 MAPWLQLCSVPFTVNACLNG......CKADLGCRSYTDELHAVAPL 753
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARIES

CHT.	Description	Abb07626 Human cyt	Abb07627 Human cyt	Abb07628 Human cyt	Aau09904 Human Int	Aau09953 Human Int	. Aau09954 Human Int	Human	Human	Human	Aau09957 Human Int	Aau09955 Human Int	Aau11355 Human DNA	Adb65245 Human pro	Aau04958 Human Int	Abu89705 Human int	Abu72600 Human IL-	Ada43241 Human int	Ada49782 Human int	Ada26975 Human PRO	Adb66909 Human PRO	Human	Adg87393 Human PRO	Adil6689 Human PRO	Adl16650 Human PRO	Ad171310 Human IL-
SUMMAKIES	QI	ABB07626	ABB07627	ABB07628	AAU09904	AAU09953	AAU09954	AAU09951	AAU09952	AAU09956	AAU09957	AAU09955	AAU11355	ADB65245	AAU04958	ABU89705	ABU72600	ADA43241	ADA49782	ADA26975	ADB66909	ABW02061	ADG87393	ADL16689	ADL16650	ADL71310
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The invention relates to an isolated cytokine receptor polypeptide designated Zcytor18. The Zcytor18 polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with psoriasis or tumour growth. The encoding nucleic acids are useful for providing Zcytor18 in vivo by gene therapy techniques. Zcytor18 oligonucleotide probes are useful for in vivo diagnosis, and the Zcytor18 probes and primers can be used to detect and localize Zcytor18 gene expression in tissue samples. The probes are also useful for detecting gross aberrations in chromosome 3 in which zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in linkage-based testing of pulmonary alveolar proteinosis, familial

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ALIGNMENTS

New cytokine receptor polypeptide designated zcytor18, useful for inhibiting cell proliferation associated with psoriasis or tumor growth, and modulating immune system by binding to endogenous zcytor18 ligand. Cytokine receptor; Zcytor18; cell proliferation; antipsoriatic; human; pulmonary alveolar proteinosis; familial periodic fever; antitumour; erythroleukemia; chromosome 3p14.3; gene therapy. Human cytokine receptor, Zcytor18 amino acid sequence. ABB07626 standard; protein; 753 AA. Gao Z; Claim 1; Page 2; 119pp; English. 23-JUL-2001; 2001WO-US023253. 26-JUL-2000; 2000US-0220747P. WPI; 2002-217048/27. N-PSDB; ABA95031, ABA95032. Kuestner RE, (first entry) (ZYMO) ZYMOGENETICS INC. WO200208259-A2. Homo sapiens. Presnell SR, 31-JAN-2002. 20-MAY-2002 ABB07626; **ABB07626**

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and
          polymorphisms of cytokine receptors.
human Zcytor18 amino acid sequence
 fever and erythroleukemia,
                                                                  100.0%;
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Human cytokine receptor, Zcytor18 variant sequence.

ABB07627 standard; protein; 753

RESULT 2

ABB07627

ABB07627
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The invention relates to an isolated cytokine receptor polypeptide designated Zcytor18. The Zcytor18 polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with psoriaais or tumour growth. The encoding nucleic acids are useful for providing Zcytor18 in vivo by gene therapy techniques. Zcytor18 oligomucleotide probes are useful for in vivo diagnosis, and the Zcytor18 probes and primers can be used to detect and localize Zcytor18 gene expression in tissue samples. The probes are also useful for detecting gross aberrations in chromosome 3 in which linkage-based testing of pulmonary alveolar proteinosis, familial periodic fever and erythroleukemia, and erythroleukemia associated with polymorphisms of cytokine receptors. The present sequence represents a human Zcytor18 variant amino acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New cytokine receptor polypeptide designated zcytor18, useful for inhibiting cell proliferation associated with psoriasis or tumor growth, and modulating immune system by binding to endogenous zcytor18 ligand.
Cytokine receptor; Zcytor18; cell proliferation; antipsoriatic; human; pulmonary alveolar proteinosis; familial periodic fever; antitumour; erythroleukemia; chromosome 3p14.3; gene therapy; variant.
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Pred. No. 0;
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                                                                                                   Location/Qualifiers
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Misc-difference 750
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inhibiting cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New cytokine receptor polypeptide designated zcytor18, useful for inhibiting cell proliferation associated with psoriasis or tumor growth, and modulating immune system by binding to endogenous zcytor18 ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytokine receptor; Zcytor18; cell proliferation; antipsoriatic; human; pulmonary alveolar proteinosis; familial periodic fever; antitumour; erythroleukemia; chromosome 3p14.3; gene therapy; splice variant.
                                                                                                                    LPRERLRPRPKVFLCYSSKDGQNHMVVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQRE
                                                                                                        WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQ
                                                                                                                                              SSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTR
                                                                                                                                                         VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAALQPL
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                             LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQQENIYSHLDBESSESSTYTAA
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N-PSDB; ABA95035, ABA95036.
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The invention relates to an isolated cytokine receptor polypeptide designated Zcytor18. The Zcytor18 polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhbit cell proliferation associated with psoriasis or tumour growth. The encoding nucleic acids are useful for providing Zcytor18 in vivo by gene therapy techniques. Zcytor18 pixobes and primers can be used to detect and localize Zcytor18 probes and primers can be used to detect and localize Zcytor18 gross aberrations in chromosome 3 in which linkage-based testing of pulmonary alveolar proteinosis, familial periodic fever and erythroleukemia yaveolar proteinosis, familial polymorphisms of cytokine receptors. The prosess and numan Zcytor18 splice variant
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98.1%;
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Matches 739; Conservative
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The invention describes novel nucleic acids encoding interleukin (IL) 17
receptor like polypeptides useful as vaccines and in gene therapy. These
receptor like polypeptides useful as vaccines and in gene therapy. These
contemporation, anti-inflammatory, and optical, anti-inflammatory and optical activities. The IL-17 receptor like nucleic acids and proteins may be used to prevent and treat diseases associated with crampinal rejection), infections (e.g. inflammation, diabetes and transplant rejection), infections (e.g. hepatitis and septicaemia), weight disorders (e.g. anorexia, cachexia and obesity), neuronal dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy), lung disorders (e.g. anorexia, cachexia and obesity), neuronal dysfunction (e.g. anorexia, cachexia and obesity), neuronal dysfunction (e.g. anorexia, cachexia and obesity), neuronal dysfunction (e.g. anorexia, cachexia and mepilepsy), bone diseases (e.g. cystic fibrosis, asthma and emphysemal, skin disease (e.g. stroke and atherosclerosis, cancers (e.g. glaucoma and retinity and encett and miscarriage), eye disorders (e.g. glaucoma and retinity and tis complements may also used as diagnostic probes to detect and miscarriage), eye disorders (e.g. glaucoma and retinial murchater the presence of similar nucleic acids in samples and its complements may also used as diagnostic probes to detect and catherise seeding restorative therapy. The ILI7Tip may also be used as anti-infertion and activity. This is the main and activity. The anti-inference of the mman activity and section and activity. This is the main and activity. This is the main activity. The mine and explained expression and activity is the protein described in the method of the inference of the method of the inference of the method of
                                                                                                                                                                                                                                                                                                                                                                                                                              anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial; hepatic; anabolic; ancectic; anti-alzheimer's; anti-parkinsonian; anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic; vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological; hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease; bone disease; vascular disorder; eye disorder; cancer; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psoriasis and glaucoma.
                                                                                                                                                                                                                                                                                                                                                                                             Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
                                                                                                                                                                                                                                                                                                              Human Interleukin 17 (hIL-17) receptor like protein.
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                                                                          AAU09904 standard; protein; 738 AA
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28-NOV-2000; 2000US-00724460.
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                                                         1 MAPWLQLCSVPFTVNACLNGSQLAVAAGGSGRARGADTCGWRMKAAARPRLCVANEGVGP
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 Length 738;
                            Indels
                                                                               MAPWLQLCSVFFTVNACLNGSQLAVAAGGSGRAWGVDTCGWR
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Query Match
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Matches 734; Conservative
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The invention describes novel nucleic acids encoding interleukin (IL) 17 receptor like polypeptides useful as vaccines and in gene therapy. These have immunomodulatory, anti-inflammatory, anti-indiabetic, anti-inforcibial, immunomodulatory, anti-inflammatory, anti-indiabetic, anti-inforcibial, anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological, osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and opticible may be used to prevent and treat diseases associated with inspropriate IL-17 receptor like polypeptide (IL17rlp) expression. These include, for example immune disorders (e.g. inflammation, diabetes and transplant rejection), infections (e.g. hepatitis and septicaemia), weight disorders (e.g. anorexia, cachexia and obesity), neuronal cysticic participates (e.g. anorexia, cachexia and obesity), neuronal cysticic fibrosis, asthma and emphysema), skin disease (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis), obne diseases (e.g. osteoporosis, asthma and emphysema), skin disease (e.g. stroke and atherosclerosis, cancers (e.g. lung disorders (e.g. elacomia, myeloma and breast cancer), reproductive disorders (e.g. lung disorders (e.g. glamcoma and retinal neuropathy). The miscarriage), eye disorders (e.g. glamcoma and retinal neuropathy cynantiate the presence of similar nucleic acids in samples and identify modulators of expression and activity. The anti-cynantian in the production of antibodies against the proteins and antagonists may also be used to down regulate cynthy neuropodies and antagonists may also be used to down regulate cynthy neuropodies and antagonists may also be used to down regulate cynthy neuropodies and antagonists may also be used to down regulate cynthy neuropodies and antagonists may also be used to down regulate cynthy neuropodies and antagonists may also be used to down regulate cynthy neuropodies and antagonists may also be used to down regulate cynthy neuropodies and antagonists may also be used to down regulate cynthy and protein seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes,
hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
bone disease; vascular disorder; eye disorder; cancer; human; mutant;
                                                                                                                                                                                                      /label= Ser, Thr, Ala, Cys
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28-NOV-2000;
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                                 PLKGFRVILEELKSEGROCOOLILKDPKOLNSSFKRTGMESOPFLNMKFETDYFVKVVPF
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Query Match
Best Local Similarity 97.5
Matches 733; Conservative

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Interleukin 17; hIL-17 receptor like protein; immunomodulatory; anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial; hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian; anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic; vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological; hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease; bone disease; vascular disorder; eye disorder; cancer; human; mutant;
                           227 FRFFYLHYKLKHEGPFKRKTCKQEQTTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA 286
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28-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention describes novel nucleic acids encoding interleukin (IL) 17
receptor like polypeptides useful as vaccines and in gene therapy. These
receptor like polypeptides useful as vaccines and in gene therapy. These
conventional and the inflammatory, anti-diabetic, anti-alzheimer's, renal,
immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
costeopathic, vascular, cytostatic, anti-laukaemic, anti-infertility and
copthalmological activities. The IL-17 receptor like nucleic acids and
copthalmological activities. The IL-17 receptor like polypeptide (IL17TIp) expression. These
inappropriate IL-17 receptor like polypeptide (IL17TIp) expression. These
cinclude, for example immune disorders (e.g. inflammation, diabetes and
cransplant rejection), infections (e.g. hepatitis and septicaemia),
conclude, for example immune disorders (e.g. patients), neuronal
dysfunction (e.g. alzheimer's disease, Parkinson's disease and epilepsy),
clung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
(e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
bone diseases (e.g. osteoporosis and hypercalcemia), wascular disorders
(e.g. stroke and arberosclarosis, cancers (e.g. lukemia, myeloma and
breast cancer), reproductive disorders (e.g. lufertility and
considers (e.g. sproduction disorders (e.g. lufertility and
considers (e.g. sproduction of similar nucleic acids in samples and identify
complements mediang restorative therapy. The IL17Th may also be used as
cantigens in the production of antibodies against the proteins and
antigens in the production of antibodies against the proteins and
antigens in the production of antibodies against the proteins and activity. Note: This aguence of specification but is based on the human Interleukin 17 (IL-17) receptor
cyckersesion and activity. Note: This sequence is not given in the
cyckersesion and activity. Note: This sequence is not given in the
cyckersesion and activity.
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                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes,
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Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 21; Page; 158pp; English.
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                                                                                                                                           16-MAR-2000; 2000US-0189816P.
28-NOV-2000; 2000US-00724460.
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97.5%;
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psoriasis and glaucoma,
                                                                                                                                                                                                                                                                                                               WPI; 2001-611392/70.
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Best Local Similarity
Matches 733; Conserv
                                                                                                                                                                                                                   (AMGE-) AMGEN INC
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WO200168859-A2
                                               20-SEP-2001
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The invention describes novel nucleic acids encoding interleukin (IL) 17

receptor like polypeptides useful as vaccines and in gene therapy. These

receptor like polypeptides useful as vaccines and in gene therapy. These

C mamunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,

immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimar's, renal,

c anti-parkinsonian, anti-convulsant, anti-aleukaemic, dermatological,

osteopathic, vascular, cytostatic, anti-leukaemic, anti-infermility and

optobhablamological, activities. The IL-17 receptor like nucleic acids and

c proteins may be used to prevent and treat diseases associated with

c proteins may be used to prevent and treat diseases associated with

c proteins may be used to prevent and field [IL171p) expression. These

c include, for axample immune disorders (e.g. inflammation, diabetes and

c transplant rejection), infections (e.g. hepatitis and septicaemia),

c include, for axample immune disorders (e.g. papatitis and septicaemia),

c weight disorders (e.g. anorexia, cachexia and obesity), neuronal

c transplant rejection), infections (e.g. papatitis and septicaemia),

c dysfunction (e.g. Alzaheimer's disease, Parkinson's disease and

c dysfunction (e.g. Alzaheimer's disease, Parkinson's disease (e.g. glomerulonephritis),

c lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease

c stroke and atherosclerosis, cancers (e.g. glomerulonephritis),

bone diseases (e.g. cystic disorders (e.g. infertility and

c breast cancer), reproductive disorders (e.g. infertility and

c presence of similar nucleic acids in samples and identify

c patients needing restorative therapy. The IL17tlp may also be used as

c antigens in the production of antibodies against the proteins and anti-

c assays to identify modulators of expression and activity. The anti-

c assays to identify modulators of expression and activity. Note assays to identify modulators of expression and activity Note: This sequence is not given in the

c specification piu
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                                                                                                                        Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psoriasis and glaucoma.
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                                                                                                                                                                                                                    Claim 18; Page; 158pp; English.
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Best Local Similarity
Matches 733; Conserv
(AMGE-) AMGEN INC
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anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial; hepatic; anabolic; ancectic; anti-alzheimer's; anti-parkinsonian; anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic; vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological; hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease; bone disease; vascular disorder; eye disorder; cancer; human; mutant; 706 480 466 540 526 900 586 99 646 720 Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psoriasis and glaucoma. WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGRGSGKGELFLVAVSAIAEKLRQAKQ QCSRRNYFRGKSGRSLXVA.CNMIQFIDEEPDWFEKQFVPFHPPPLRYREPVLEKFDSGL VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAALQPL 587 VLNDVMCKPGPESDFCLKVEAPVLGATGPADSQHESQHGGLDQDGEARPALDGSAALQPL LHTVKAGSPSDMPRDSG1YDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSSGLGEEE SSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTR SSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTR Human Interleukin 17 (hIL-17) receptor like protein substitution #2. Interleukin 17; hIL-17 receptor like protein; immunomodulatory; Tyr Ala, PPALPSKLLSSGSCKADLGCRSYTDELHAVAP 738 /label= Phe, Leu, Val, Ile, PPALPSKLLSSGSCKADLGCRSYTDELHAVAP Location/Qualifiers Ź AAU09952 standard; protein; 738 16-MAR-2000; 2000US-0189816P. 28-NOV-2000; 2000US-00724460. 15-MAR-2001; 2001WO-US008678 (first entry) WPI; 2001-611392/70. (AMGE-) AMGEN INC Key Misc-difference WO200168859-A2. Homo sapiens. 14-FEB-2002 20-SEP-2001 Synthetic AAU09952; 347 407 481 467 541 527 601 199 647 721 707 421 mutein. Jing S; RESULT 8 ð d g 셤 ò 셤 à 셤 8 원 8 ò

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                                                                                         receptor like polypeptides useful as vaccines and in gene therapy. These have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial, anti-parkinsonian, anti-inflammatory, anti-diabetic, anti-microbial, anti-parkinsonian, anti-convulsant, anti-athmatic, anti-microbial, anti-parkinsonian, anti-convulsant, anti-leukaemic, anti-infertility and optical activities. The IL-17 receptor like nucleic acids and proteins may be used to prevent and treat diseases associated with inappropriate IL-17 receptor like polypeptide (ILI7TP) expression. These inappropriate IL-17 receptor like polypeptide (ILI7TP) expression. These include, for example immune disorders (e.g. inflammation, diabetes and transplant rejection), infections (e.g. hepatitis and septicaemia), weight disorders (e.g. anorexia, cachexia and obesity), neuronal dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy), dugfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy), tung disorders (e.g. cystic fibrosis, asthma and emphysemal, skin disease (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis), bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders (e.g. etroke and atheroselerosis, cancers (e.g. infertility and breast cancer), reproductive disorders (e.g. infertility and current presence of similar nucleic acids in samples and identify patients needing restorative therapy. The ILI7Tip may also be used as antigens in the production of antibodies against the proteins and in cultivity. Modulators of expression and activity. Note: This sequence is not given in the expression and activity. Note: This sequence is not given in the expression and activity. Note: This sequence is not given in the production of the human interlement in the human interpetable of the human interpetable 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKPRNLNISQHGSDMQVSFDHAPHNFG 226
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                                                                          invention describes novel nucleic acids encoding interleukin (IL) 17
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Claim 19; Page; 158pp; English.
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733; Conservative
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Best Local &
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anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic; vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological; hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
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                                                                                                                                                                                  646
                                                                                                                                                                                                                                            720
                                                                                                                                                                                                                                                                                                         706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psoriasis and glaucoma.
                                                                                                                                                                                                                                            LHTVKAGSPSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSSGLGEEE
                                                                                                                                                                                                                                                                                   LHTVKAGSPSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSGLGEEE
                                QGSRRNYFRSKSGRSLYVAI CNMHQFIDEEPDWFEKQFVPFHPPPLRYREPVLBKFDSGL
                                                                                                                    VI,NDVMCKPGPESDFCLKVEAAVLGATGPADSOHESOHGGLDODGEARPALDGSAALQPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bone disease; vascular disorder; eye disorder; cancer; human; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interleukin 17; hIL-17 receptor like protein; immunomodulatory; anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial; hepatic; anabolic; ancectic; anti-alzheimer's; anti-parkinsonian;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Interleukin 17 (hIL-17) receptor like protein substitution #6.
                                                                                                                                                                                                                                                                                                                                                                                                                    PPALPSKLLSSGSCKADLGCRSYTDELHAVAP 738
                                                                                                                                                                                                                                                                                                                                                                    PPALPSKLLSSGSCKADLGCRSYTDELHAVAP 752
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inciprovinted that the purpopution (111) represent the control of inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. information given in claim 23

Sequence 738 AA;

Gaps 4; Indels 14; 4; Length 738; 8 Mismatches Score 3894; Pred. No. 0; 1; 97.0%; Conservative Similarity 733; Query Match Local Matches

1 MAPWLQLCSVFFTVNACLNGSQLAVAAGGSGRARGADTCGWRMKAAARPRLCVANEGVGP

46 dSvS-----1 MAPWLQLCSVFFTVNACLNGSQLAVAAGGSGRAWGVDTCGWR----

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360 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQQENIYSHLDEESSESSTYTAA 301

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WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQ SSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTR SSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMDNLPQLCSHLHSRXHGLQEPGQHTR 407 481 467

526 900

GGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFEKQFVPFHPPPLRYREPVLEKFDSGL

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661 LHTVKAGSPSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSSGLGEEE 720

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Æ. AAU09957 standard; protein; 738

AAU09957;

(first entry) 14-FEB-2002 Human Interleukin 17 (hIL-17) receptor like protein substitution #7.

Interleukin 17; hIL-17 receptor like protein; immunomodulatory; anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial; hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian; anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic; vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological; hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease; bone disease; vascular disorder; eye disorder; cancer; human; mutant; mutein.

sapiens. Synthetic. Homo

/label= Cys, Ala, Ser Location/Qualifiers Misc-difference 602

WO200168859-A2

20-SEP-2001

15-MAR-2001; 2001WO-US008678

16-MAR-2000; 2000US-0189816P. 28-NOV-2000; 2000US-00724460.

(AMGE-) AMGEN INC

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WPI; 2001-611392/70.

Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psoriasis and glaucoma.

Claim 24; Page; 158pp; English.

The invention describes novel nucleic acids encoding interleukin (IL) 17

receptor like polypeptides useful as vaccines and in gene therapy. These
have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
immunosuppressive, hepatic, anabolic, anorectic, anti-latheimer's, renal,
continuous anti-convulsant, anti-sethmatic, dermatological,
anti-parkinsonian, anti-convulsant, anti-leukaemic, anti-infertility and
costeopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and
costeopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and
coptinal mological activities. The IL-17 receptor like nucleic acids and
coptinal may be used to prevent and treat diseases associated with
controlled, for example immune disorders (e.g. inflammation, diabetes and
controlled, for example immune disorders (e.g. inflammation, diabetes and
controlled, for example immune disorders (e.g. inflammation, diabetes and
controlled, for example immune disorders (e.g. inflammation, diabetes and
controlled, for example immune disorders (e.g. cystic fibrosis, asthma and cophysema),
controlled, for example immune disorders (e.g. cystic fibrosis, asthma and emphysema),
controlled, for example immune disorders (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and
controlled, for example immune disorders (e.g. infertility and
controlled), reproductive disorders (e.g. infertility and
controlled), reproductive disorders (e.g. infertility and

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ASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVTILWSPGALGIE 106
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miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The DNA and its complements may also used as diagnostic probes to detect and quantitate the presence of similar nucleic acids in samples and identify patients needing restorative therapy. The ILI/Thp may also be used as antigens in the production of antibodies against the proteins and in assays to identify modulators of expression and activity. The anti-ILI/Thp antibodies and antagonists may also be used to down regulate expression and activity. Note: This sequence is not given in the specification but is based on the human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904) and has been created according to
                                                                                                                                                                                                                                                                                                                                                                           1 MAPWLQLCSVFFTVNACLNGSQLAVAAGGSGRAWGVDTCGWR------GVGP 46
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Best Local Similarity 97.5%;
Matches 733; Conservative
                                                                                                                                                                                                                             Sequence 738 AA;
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Interleukin 17; hIL-17 receptor like protein; immunomodulatory; anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial; hepatic; anabolic; ancectic; anti-alzhaimer's; anti-parkinsonian; anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic; vascular; cytostatic; anti-leuksemic; anti-infertility; ophthalmological; hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
                                                                                                                     bone disease; vascular disorder; eye disorder; cancer; human; mutant
                                                 Human Interleukin 17 (hIL-17) receptor like protein substitution #5.
                                                                                                                                                                                        /label= Cys, Ser, Ala
                                                                                                                                                                       Location/Qualifiers
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AAU09955 standard; protein; 738
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28-NOV-2000; 2000US-00724460
                                                                                                                                                                                                                                         15-MAR-2001; 2001WO-US008678
                                 (first entry)
                                                                                                                                                                                                                                                                                    (AMGE-) AMGEN INC.
                                                                                                                                                                                 Misc-difference
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                                                                                                                                               sapiens
                                 14-FEB-2002
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                                                                                                                                                        Synthetic.
                 AAU09955;
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Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psoriasis and glaucoma.

WPI; 2001-611392/70.

Claim 22; Page; 158pp; English.

The invention describes novel nucleic acids encoding interleukin (IL) 17

receptor like polypeptides useful as vaccines and in gene therapy. These

creceptor like polypeptides useful as vaccines and in gene therapy. These

contemporate inflammatory, anti-alabeimer's, renal,

immunosuppressive, hepatic, anabolic, anorectic, anti-alabeimer's, renal,

anti-parkinsonian, anti-convulsant, anti-alabeimer's, renal,

costeopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and

opticins may be used to prevent and treat diseases associated with

copticins may be used to prevent and treat diseases associated with

inappropriate IL-17 receptor like polypeptide (IL17Th) expression. These

cransplant rejection), infections (e.g. hepatitis and septicaemia),

weight disorders (e.g. alorexia, cachexia and obesity), neuronal

dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),

cup disorders (e.g. anorexia, cachexia and obesity), neuronal

dysfunction (e.g. alzheimer's disease, Parkinson's disease and epilepsy),

cup disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease

(e.g. stroke and therosclerosis, and hypercalcaemia), wascular disorders

(e.g. stroke and atherosclerosis, and retinal neuropathy). The

miscarriage), reproductive disorders (e.g. leukemia, myeloma and

breast cancer), reproductive disorders (e.g. leukemia, and its complements may also used as diagnostic probes to detect and

cynticians in the production of sntibodies as against the proteins and in

assays to identify modulators of expression and activity. The anti
cyntry antipodies and antagonists may also be used as controlled assays to identify modulators of expression and activity. Note: This sequence is not given in the

cyntrication but is based on the human Interleukin 17 (IL-17) receptor

like protein sequence (AMU09904) and has been created according to

RESULT 11 AAU09955

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Misc-difference
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                                                                      ASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVTILWSPGALGIE
                                                                                                   FLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFKRTGMESQPFLNMKFETDYFVKVVPF
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                                              Gaps
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                                             14;
                              Length 738;
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Pred. No. 0;
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in claim 22
                              96.98;
97.58;
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                                      al Similarity 97.5
733; Conservative
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 information given
                Sequence 738 AA;
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The invention relates to primate and rodent DNAX cytokine receptor subbunit (DCRS) polypeptides and the polyunclectides encoding them. The receptors, or their portions may be useful as phosphate labelling enzymes to label general or specific substrates. The subunits may also be functional immunogens to elicit recognising antibodies, or antigens capable of binding antibodies. A combination, e.g., including a DCRS can be used as an immunogen for the production of antisera or antibodies capable of distinguishing between other cytokine receptor family members. A purified DCRS can also be used as a reagent to detect antibodies generated in response to the presence of elevated levels of expression, or immunological disorders which lead to antibody production to the endogenous receptor. This sequence represents the human DCRSB polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVTILWSPGALGIE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide useful for detecting antibodies generated in response to presence of increased protein levels or immunological disorders.
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Pred. No. 0;
2; Mismatches
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Location/Qualifiers
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/note= "Encoded
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96.3%;
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cell regeneration; membrane protein; signal transduction-related protein;
transcription-related protein; osteoporosis; neurological disease;
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Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAALQPL 645
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WVIQKIHESQFIIVVCSKGMKYPVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQ
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(REAS-) RES ASSOC BIOTECHNOLOGY.
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25-JAN-2002; 2002US-00350978.
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O J, Isono Y, H
Yoshikawa T, O
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or its partial peptide, an antibody binding to the polypeptide or cof the polymuclectide, immunologically assaying the polypeptide or peptide of peptide of the polymuclectide by contexting the polypeptide or peptide of with the antibody of the encoded protein, and observing the binding between the two, a transformant carrying the polymuclectide in an expressible manner and an antisense polymuclectide. The oligonuclectide of su suseful as a primer for synthesising the polymuclectide, or as a probe for detecting the polymuclactide. The polymuclectide, or as a probe of proteins are useful as pharmaceutical agents and many disease-related proteins are useful as pharmaceutical agents and activity, or as targets of genes may be included in them, for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy. The genes are involved in tissue and/or call regeneration. Membrane proteins, signal transduction-related proteins, cranscription-related proteins, disease-related proteins and genes encoding them can be used as indicators for diseases (e.g. osteoporosis, cancer, tumours. The cDNA may be used to regulate the activity or expression of the encoded protein to treat diseases. The sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office.
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716 LGEEEPPALPSKLLSSGSCKADLGCRSYTDELHAVAPL 753

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101 ACHDOVAVTILWSPGALGIEFLKGFRVILEELKSEGROCOQLILKDPKQLNSSFKRTGME 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SQPFLNMKFETDYFVKVVPFPSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKPRNLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 RMKAAARPRLCVANE-GVGPASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNITISQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISQ-------HGSDMQVSPDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 96.0
Matches 702; Conservative
                                                                                                                                                                                                                                                (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                               2001-451708/48.
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                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAS09517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 728 AA;
                                                                                                        02-JUN-2000; 2
22-JUN-2000; 2
22-AUG-2000; 2
                                           18-FEB-2000;
02-MAR-2000;
21-MAR-2000;
21-MAR-2000;
                                                                                                                                                                                                                                                                                                Gurney AL, L
Watanabe CK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "cAMP/GMP-dependent protein kinase phosphorylation
                                                                                                                                                                                                                 Human; Interleukin-17 receptor; IL-17RH4; agonist; antagonist; PRO20026; DNA 154095-2998; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; diabetes mellitus; allergic disease; asthma; demyelinating disease; degenerative cartilaginous disorder; transplantation associated disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116. 424
/note= "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Glycosaminoglycan attachment site"
38. .41
/note= "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          66. 59
note= "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "Asn is N-glycosylated"
47. .150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182. .185
/note= "Asn is N-glycosylated"
232. .235
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note= "N-myristoylation site"
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note= "N-myristoylation site"
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312. .319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "N-myristoylation
                                                                                                                                                                                         Human Interleukin 17 receptor, IL-17RH4.
                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                              AAU04958 standard; protein;
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/note= "N
32
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/note= "W
74
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/note= "N-1
652. .657
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/note= "Gl
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/note= "N-
                                                                                                                                                            entry)
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/note= "
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                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                   691
                                                                                                                           AAU04958;
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AAU04458
AAX
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Homo
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62

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The sequence is PRO20026 which is the human Interleukin 17 receptor, IL-
17RH4, encoded by DNA 154095-2998. A composition containing ant/agonists
to the PRO polypeptides or individual components are useful for treating
a mammal with an immune related disease, e.g. systemic lupus
erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic
arthritis, a spondyloarthropathy, systemic sclerosis, an idiopathic
inflammatory myopathy, Sjogren's syndrome, systemic vasculitis,
sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia,
thyroiditis, diabetes mellitus, immune-mediated renal disease, a
demyelinating disease, an autoimmune or immune-mediated skin disease,
contact dermatitis, an allergic disease, e.g. food hypersensitivity,
asthma, a transplantation associated disease, or a chronic inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          demyelinating polyneuropathy. Treating a degenerative cartilaginous disorder comprises administering a PRO1031 or PRO1122 polypeptide agonist, or antagonist to the mammal. Numerous examples of the diseases and disorders are given in the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Grimaldi CJ;
Vandlen RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel PRO polypeptides homologous to interleukin-17, useful for the diagnosis and treatment of immune related disease e.g. rheumatoid arthritis and diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Filvaroff E, Fong S, Goddard A, Godowski PJ,
J, Li H, Hillan KJ, Tumas D, Van Lookeren M,
CK, Williams PM, Wood WI, Yansura DG;
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96.7%; Pred. No. 0;
ive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 10; Fig 18; 188pp; English.
                                                                                                                                    2000WO-US007532.
2000WO-US015264.
2000US-0213807P.
2000US-00644848.
                                                                                                                                                                                                                                                                             24-AUG-2000; 2000WG-US023328.
24-OCT-2000; 2000UG-0242837P.
10-NOV-2000; 2000UG-0253845P.
28-NOV-2000; 2000UG-0253646P.
01-DEC-2000; 2000WG-US032678.
                                 2000WO-US004341.
2000WO-US005841.
2000US-0191007P.
2000US-0175481P
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ATLPTVMCRKKQQENIYSHLDEESSESSTYTAALPRERLRPRPKVFLCYSSKDGQNHMNV 362
                                                                       VQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQKIHESQPIIVVCSKGMKYFVDKK 422
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                                                        VQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQKIHESQFIIVVCSKGMKYFVDKK 447
                                                                                                                  NYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILD 507
                                                                                                                                                                                                                                                                                                                      GPADSOHESOHGGLDODGEARPALDGSAALQPLLHTVKAGSPSDMPRDSGIYDSSVPSSE 662
                                                                                                                                                                                                                                                                                                                                                      LSLPLMEGLSTDQTETSSLTESVSSSGLGEEEPPALPSKLLSSGSCKADLGCRSYTDEL 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; interleukin 17; IL-17; IL17 receptor; angiogenesis; T-lymphocyte proliferation; inflammatory cell infiltration; immune related disorder; systemic lupus erythematosus; osteoarthritis; rhumatoid arthritis; spondyloarthropathy; systemic solerosis; Sjogren's syndrome; sarcoidosis; autoimmune haemolytic anaemia; thyroiditis; diabetes mellitus; immune-mediated renal disease; demyelinating disease; Goullain-Barre syndrome; hepatobiliary disease; hepatitis; inflammatory bowel disease; Whipple's disease; psoriasis; immune-mediated skin disease; erythema multiforme; contact dermatitis; allergic disease; asthma; atopic dermatitis; decontact dermatitis; urticaria; immunologic disease of the lung; eosinophilic pneumonia; idiopathic pulmonary fibrosis; transplantation associated disease;
                                                                                                                                                                                                                                                   LSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNMHQFI
                                                                                                                                                                                            LSTKYRLMDNL-PQLCSHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNMHQFI
                                                                                                                                                                                                                                  DEEPDWFEKQFVPFHPPPLRYREPVLEKFDSGLVLNDVMCKPGPESDFCLKVEAAVLGAT
                                                                                                                                                                                                                                                                                            GPADSQHESQHGGLDQDGEARPALDGSAALQPLLHTVKAGSPSDMPRDSGIYDSSVPSSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABU89705 standard; protein; 728 AA
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99WO-US005028.
99US-0131022P.
99US-0131022P.
99US-00311832.
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26-APR-1999;
14-MAY-1999;
14-MAY-1999;
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08-MAR-1999;
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                            303
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2000WO-US015264
2000US-0213807P
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2000WO-US034956
                                                       2000US-0175481P
                                                                    2000WO-US004341
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14-MAY-1999;
09-JUN-1999;
23-DEC-1999;
30-DEC-1999;
11-JAN-2000;
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                                                                  18-FEB-2000;
01-MAR-2000;
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21-MAR-2000;
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24-OCT-2000;
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20-DEC-2000
                                                                                                                                                                                                           10-NOV-2000
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(GETH) GENENTECH INC.

ΰ Chen J, Filvaroff E, Fong S, Goddard A, Godowski P, Grimaldi Gurney A, Li H, Hillan K, Tumas D, Vanlookeren M, Vandlen R; Watanabe C, Williams PM, Wood WI, Yansura D;

WPI; 2003-428843/40. N-PSDB; ACA89858 New PRO polypeptides and polynucleotides homologous to interleukin-17, useful for treating e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, or systemic sclerosis

Claim 10; Fig 18; 129pp; English.

The invention relates to a nucleic acid having similarity to interleukin
(C 17 (IL-17) or IL-17 receptor comprises at least 80% nucleic acid sequence
clantity to a nuclectide sequence which: (a) encodes a polypeptide having
a sequence of appearing as ABUB969708 and ABUB9708-ABUB9701
(C 18), lacking or having its associated signal peptide; (b) encodes an

(C 2), lacking or having its associated signal peptide; (c)

(C 2) consists of a sequence of appearing as ACAB9850-ACAB9855
(C 2) consists of a sequence of appearing as ACAB9850-ACAB9855
(C 3) consists of the full-length coding sequence of

(C 3) consists of the cDNA deposited under ATCC accession

(C 3) consists of the cDNA deposited under ATCC accession

(C 4) consists of the cDNA deposited under ATCC accession

(C 5) consists of the cDNA deposited under ATCC accession

(C 5) consists of the cDNA deposited under ATCC accession

(C 6) consists of the cDNA deposited under ATCC accession

(C 6) consists of an activity (or mimicking the polypeptides or ant/Agonists, enhancing the infiltration of for inflammatory cells into a tissue of a mammal by administering a PRO1031 polypeptide, its ant/Agonist or an anti-PRO1031

(C 6) consistering a PRO1031 polypeptide, its ant/Agonist or an anti-PRO1031

(C 6) consistering a PRO1031 polypeptide, its ant/Agonist or an anti-PRO1031

(C 6) construction of an activity (or acti chronic inflammatory demyelinating polyneuropathy, a hepatobiliary chronic inflammatory demyelinating polyneuropathy, a hepatobiliary disease, infectious or autoimmune chronic active hepatitis, primary billary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease, gluten-sensitive enteropathy, Mhipple's disease, an autoimmune or immune-mediated skin disease, a bullous skin disease, erythema multiforme, contact dermatitis, psoriasis, an allergic disease, asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity, urticaria, an immunologic disease of the lung,

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eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, a transplantation associated disease, graft rejection or graft-versus-host disease. The present sequence represents an IL17 or IL17 receptor homologue of the invention
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                      - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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4013
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Perfect score:
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Result

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Sequence 20, Appl
Sequence 30, Appl
Sequence 303, App
Sequence 303, App
Sequence 6384, Ap
Sequence 25826, A
Sequence 9916, Ap
Sequence 1916, Ap
                                                                                                                                                                 Sequence 3, Appli
Sequence 3, Appli
Sequence 664, App
Sequence 6898, Ap
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                              US-08-449-645A-20
US-08-702-367A-20
US-08-702-367A-20
US-09-188-930-303
US-09-949-016-6384
US-09-949-016-9916
US-09-949-016-9916
US-09-949-016-9917
US-09-949-016-10562
US-09-949-016-016-019
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ALIGNMENTS

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APPLICANT: Wandlookers, Mallookers, Malloo
Sequence 18, Application US/09747259
Patent No. 6569645
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Chen, Jian
APPLICANT: Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Godowski, Paul
Grimaldi, Christopher
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US-09-816-744-18
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                                                                                                                                                                            Length 728;
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                                                                                                                                                                          Query Match 92.3%; Score 3703;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 702; Conservative 2; Mismatches
PRIOR APPLICATION NUMBER: US 60/242,837
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: PCT/US00/30873
PRIOR FILING DATE: 2000-11-10
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
PRIOR FILING DATE: 2000-12-01
PRIOR FILING DATE: 2000-12-01
SEQ ID NO 18
                                                                                                                              TYPE: PRT
ORGANISM: Homo Sapien
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HAVAPL 728
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RESULT 2

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                                                                                                                                                              APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul
APPLICANT: Goddwski, Paul
APPLICANT: Gurney, Austin
APPLICANT: Gurney, Austin
APPLICANT: Gurney, Austin
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Vanicokeren, Menno
APPLICANT: Vandlen, Richard
APPLICANT: Watanabe, Colin
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Sequence 18, Application US/09816744
Patent No. 6579520
GENERAL INFORMATION:
                                                                                                          APPLICANT: Chen, Jian APPLICANT: Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo Sapien
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Best Local Similarity
Matches 702; Conserv
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114 -PGALGIEFLKGFRVILEELKSEGROCOQLILKDPKOLNSSFKRTGMESQPFLNMKFETD 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        549 RSKSGRSLYVAICNMHQFIDEEPDWFE-----KQFVPFHPPPLRYREPVLEKFDSGL
                                                                          YFVKV--VPFPSIKNESNYHPFFFRTRACDLLLQPDNLACK---PFWKPRNL--
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Bacter No. 6072033
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
NUMBER OF SEQUENCES:
ADDRESSEE: Immunex Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: Apple Operating System 7.5.5 SOFTWARE: Microsoft Word for Apple, Version 6.0.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/022,255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operatir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Immunex Corporation
STREET: 51 University Street
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MEDIUM TYPE: Floppy
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                                                                                                                                                            LSLPLMEGLSTDQTETSSLTESVSSSGLGEEEPPALPSKLLSSGSCKADLGCRSYTDEL 747
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                                                                                                                                                                                                                                                                                                                                        Sequence 10. Application US/08620694A
Patent No. 5869286
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 7.8%; Score 312; DB 2; Length 866; Best Local Similarity 23.1%; Pred. No. 3.8e-23; Matches 178; Conservative 107; Mismatches 338; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694A
FILING DATE: 21 MARCH 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA: APPLICATION DATA: 7 AUGUST 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION WINBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION: NAME: Perkins, PALTICIA Anne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REPERENCE/DOCKET NUMBER: 2617
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 51 University Street CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 866 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
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US-08-620-694A-10
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173 YPVKV--VPFPSIKNESNYHPFFFRTRACDLLLQPDNLACK---PFWKPRNL----- 219
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641 IDQDGEARPALDGSA---ALQ-----PLLHTVKAGSPSDMPRDSGIYDSSVPSSELSLP 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 NITFKYDNC--TTYLNPVGKHVIADAQNIT-----ISQYACHDQ----VAVTILWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 - PGALGIEFLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFKRTGMESQPFLNMKFETD
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                                                                                                                                          768
                                                                                                                                                                                                                                                                                                                                APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
ITILE OF INVENTION: No. 6072037el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.8%; Score 312; DB 3; Length 866; 23.1%; Pred. No. 3.8e-23; ve 107; Mismatches 338; Indels 1.
                                                                                                                        LMEGLSTDQTETSSLTESVSSSGLGEEEPPALPSKLLSSGSCKADLGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USSN 08/410,535
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,53
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: PERKINS, PATRICIA Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELECHONE: (206)587-0430
                                                                                                                                                                                                                                                           ; Sequence 10, Application US/09022696
; Patent No. 6072037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative 107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 866 amino acids
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nes 178; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 - PGALGIEFLKGFRVILEELKSEGROCOOLILKDPKOLNSSFKRTGMESOPFLNMKFETD 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173 YFVKV--VPFPSIKNESNYHPFFFRTRACDLLLQPDNLACK---PFWKPRNL----- 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157 YEVTVHHLPKPIPDGDPNHOSKNPLVPDCEHARMKVTTPCMSSGSLWDP-NITVETLEAH 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     328 ATLFTVMCRKKQQENIYSHLDEESSESSTYTAALPRERLRPRP----KVFLCYSSKDGQN 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            384 HMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWV----IQKIHESQFIIVVCSKG 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       440 MKYFVDKKNYKHKGGG------RGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIA 491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49 NCTVKNSTCLDDSWIHP-----RNLTPSSPKDLQIQLHFAHTQGGDLFPVAHIEWT 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.8%; Score 312; DB 3; Length 866; Best Local Similarity 23.1%; Pred. No. 3.8e-23; Matches 178; Conservative 107; Mismatches 338; Indels 146;
              CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/620,694
FILING DATE: 21 MARCH 1996
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
PRIOR APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
ATTORNEY,AGENT INFORMATION:
NAME: Perkins, Patricia Anne
RECASTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / MOLECULE TYPE: protein US-09-022-255-10
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Sequence 10, Application US/09022253
Patent No. 6096305
REFERENCE/DOCKET NUMBER: 262
TELECOMMUNICATION INFORMATION:
TELEPAX: (206) 587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                 US-08-978-773-4
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                                                                                                                                                                                                                                                                                TR----AKWQALLGRGAPVRLRCDHGKPVGDLFTAAMNMILPDFKR-----PACFGTYVV 501
                                                                                                                                                                                                                                                                                                              VYF-DYSCEGDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTRQG--SRRNYF 548
                                                                                                                                                                                                                                                                                                                                  HMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWV----IQKIHESQFIIVVCSKG 439
                                                                                                                                                                                                                                                     440 MKYFVDKKNYKHKGGG------RGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIA 491
                                              QLRVSFTLWNESTHYQILLTSFPHMENHSCFEHMH-HIPAPRPEEFHQRSNVTLTLRNLK 274
                                                                           SCLLQNVSPGDYIIELVDDT---NTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 327
                                                                                                     GCCRHQVQIQPFFSSCLNDCLRHSATVSCPEMPDTPEPIPDYMPLWVYWFITGISILLVG 334
                                                                                                                                     ATLFTVMCRKKQQENIYSHLDEESSESSTYTAALPRERLRPRP----KVFLCYSSKDGQN 383
                   -----NISQHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Troutt, Anthony
TITLE OF INVENTION: Method of Regulating Nitric Oxide Production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   692 IMEGLSTDQTETSSLTESVSSSGLGEEEPPALPSKLLSSGSCKADLGC 740
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple PowerMacintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for PowerMacintosh, Version (
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,773
                                                                                                                                                                                                                                                                                                                                                                                                                                   VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHE----
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 27 NOVEMBER 1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08978773
Patent No. 6083906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216 OLRVSFTLWNESTHYOILLTSFPHMENHSCFEHMH-HIPAPRPEEFHORSNVTLTLRNLK 274
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                                                                                                                                                                                                                                                 69 NITEXYDNC--TTYLNPVGKHVIADAQNIT-----ISQYACHDQ-----VAVTILWS
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                                                                                                                                                 Length 866;
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                                                                                                                                                 Query Match 7.8%; Score 312; UB 3; L
Best Local Similarity 23.1%; Pred. No. 3.8e-23;
Matches 178; Conservative 107; Mismatches 338;
: 866 amino acids
amino acid
                                                                           MOLECULE TYPE: protein
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US-09-022-253-10
LENGTH:
TYPE: am
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335 SVILLIVCMTWRLAGPGS---EKYSDDTKYTDGLPAADLIPPPLKPRKVWIIYSA-DHPL 390
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Patent No. 6100235
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          692 IMEGLSTDQTETSSLTESVSSSGLGEEEPPALPSKLLSSGSCKADLGC
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHE--
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NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REPERENCE/DOCKET NUMBER: 2617-B
TELECOMUNICATION:
TELECOMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 51 University Street
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 06
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
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TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 10:
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                                  APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Apple Operating System 7.5.5 SOFTWARE: Microsoft Word for Apple, Version 6.0.1 CURRENT APPLICATION DATA: FILING DATE: US/09/022,253 FILING DATE: RASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 7 AUGUST 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
CLASSIFICATION:
CLASSIFICATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REGISTRATION NUMBER: 231,695
REGISTRATION NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US/08/620,694
APPLING DATE: 21-MARCH-1996
APPLICATION NUMBER: USSN 08/538,765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operati
                                                                                                                                                                                                                                                          ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7: (206)587-0430
(206)
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
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MOLECULE TYPE: protein
US-09-022-253-10
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   GENERAL INFORMATION:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Co
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (206)
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                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                           -----NISOHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTETT 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYLLLIVCMTWRLAGPGS---EKYSDDTKYTDGLPAADLIPPPLKPRKVWIIYSA-DHPL 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 440 MKYFVDKKNYKHKGGG------RGSGKGELFLVAVSAIAEKLROAKOSSSAALSKFIA 491
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"Sequence 10, Application US/09022259

"Sequence 10, Application US/09022259

"Sequence 10, Application:

APPLICANT: Yao, Zhengbin

"APPLICANT: Spriggs, Melanie

"APPLICANT: Fanalow, William

"TITLE OF INVENTION: No. 6191104e1 Receptor That Binds IL-17
                                                                                                       7.8%; Score 312; DB 3; Length 866; 23.1%; Pred. No. 3.8e-23;
                                                                                                                                  178; Conservative 107; Mismatches 338; Indels
                                                                                                                      23.1%;
      CHARACTERISTICS
                     866 amino acids
amino acid
                                             TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-260-10
                                                                                                                      Similarity
       SEQUENCE
                                                                                                          Query Match
Best Local S
Matches 178
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114 -PGALGIEFLKGFRVILEELKSEGROCQQLILKDPKQLNSSFKRTGMESQPFLNMKFETD 172
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                                                                                                                                                                                                                                                                                   SYSTEM: Apple Operating System 7.5.5
Microsoft Word for Apple, Version 6.0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USSN 08/410,535
                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/022,259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REPERENCE/DOCKET NUMBER: 2617-B
TELECOMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                          COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operatin
SOFTWARE: Microsoft Word for App
ALUKESSEB: Immunex Corporation STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 04
FILING DATE: 23 MARCH 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 866 amino acids
                                                                                                                                                                                                                               Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA
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                                                                                                                                                                  ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                          RSKSGRSLYVAICNMHQFIDEEPDWFE-----KQFVPFHPPPLRYREPVLEKFDSGL 600
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                                                                                                                                                                                                                           492 VYF-DYSCEGDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTRQG--SRRNYF 548
                                                                                                                                                                                                          LDQDGEARPALDGSA---ALQ-----PLLHTVKAGSPSDMPRDSGIYDSSVPSSELSLP 691
L--GSSTPMASPDLLPEDVR-----EHLEGLMLSLFEQSLSCOAQGGC 768
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6197525el Receptor That Binds IL-17
CORRESPONDENCE: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                               LMEGLSTDQTETSSLTESVSSSGLGEEEPPALPSKLLSSGSCKADLGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: Apple Fower Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,257
                                                                                                                                                    601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASIFICCATION:
PRIOR APPLICATION DATA:
PAPPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PILING DALL.

ATTORNEY/AGENT INFORMATION:
NAME: PERKINS, PALTICIA Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/09022257
Patent No. 6197525
GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (206)
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: protein US-09-022-257-10
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                                                                                                                                                                                                                           - PGALGIEFLKGFRVILEELKSEGROCOOLILKDPKOLNSSFKRIGMESOPFLNMKFETD 172
                                                                                                                                                                                                                                                                                100 LOTDASILYLEGAELSVLOLNTNERLCVR--FEFLSKLRHHHRRWRFTFSHFV-VDPDQE 156
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                                                                                                                                                     YFVKV--VPFPSIKNESNYHPFFFRIRACDLLLQPDNLACK---PFWKPRNL-----
                                                       Indels 146; Gaps
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Fanslow, William
TITLE OF INVENTION: No. 6680057el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
     Length 866;
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Query Match 7.8%; Score 312; DB 3; L Best Local Similarity 23.1%; Pred. No. 3.8e-23; Matches 178; Conservative 107; Mismatches 338;
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ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
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Patent No. 6680057
GENERAL INFORMATION:
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COUNTRY: USA
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Sequence 1, Application US/10033522

Patent No. 6793919

GENERAL INFORMATION:
FALLELICANT: MOHILER, Kendall M.
TITLE OF INVENTION: Methods for Treating Rheumatoid Arthritis Using IL-17 Antagonists
TITLE OF INVENTION: WASHER: US/10/033,522
CURRENT APPLICATION NUMBER: US/10/033,522
CURRENT PILING DATE: 2000-10-18
PRIOR FILING DATE: 2000-10-18
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
                                      640
                                                              LVAAVEPGPLADGAAVRLALAGEGEACPLLGSPGAG-----RNSVLF---LPVDPEDSP 727
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                                                                                                                   LDQDGEARPALDGSA---ALQ----PLLHTVKAGSPSDMPRDSGIYDSSVPSSELSLP
560 RSPGGRQLRAALDRFRDWQVRCPDWFECENLYSADDQDAPSLDEEV-FEEPLLPP-GTGI
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23.1%; Pred. No. 3.8e-23;
iive 107; Mismatches 338.
                                          VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHE --
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US-10-033-522-1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LQTDASILYLEGAELSVLQLNTNERLCVR--PEFLSKLRHHRRWRFTFSHFV-VDPDQE 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 NITEKYDNC--TTYLNPVGKHVIADAQNIT-----ISQYACHDQ-----VAVTILWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.8%; Score 312; DB 4; Length 866;
llarity 23.1%; Pred. No. 3.8e-23;
Conservative 107; Mismatches 338; Indels 146;
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                                                                                       OPERATING SYSTEM: Apple Operating System 7.5.5 SOFTWARE: Microsoft Word for Apple, Version 6.0.1
                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE: «Unknown»
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                              APPLICATION NUMBER: US/09/549,679
                                                                                                                                                                                                                                                                                                                      NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
                                                MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                    FILING DATE: 14-Apr-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                       (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 866 amino acids TYPE: amino acid
                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHARACTERISTICS
                                READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 178; Conserv
                                COMPUTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   455 AKWKAILGWAEPAVQLRCDHWKPAGDLFTAAMMILPDFKR-----PACFGTYVVCYFSG 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RSLYVAICNWHQFIDEEPDWFEKQFVPFHP----PPLR---YREPVLEKFDSGLVLNDVM 606
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                                                                                                                                                                            132 LSMLQHHRKRWRFSF----SHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKIIFVPDC 185
                                                                                                                                                                                                                                                           186 EDSKMKMTTSCVSSGSLWDP-NITVETLDTQHLRVDFTLWNESTPYQVLLESFSDSENHS 244
                                                                                                                                                                                                                                                                                                  231 SFD------HAPHNFGFRFFYLHYKLKHE---GPFKRKTCKQEQTTETTSCLL 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                            331 FTVMCRKKQQENIYSHLDEESSESTYTAALPRERLRPRPKVFLCYSSKDGQNHMNVVQC 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQK----IHESQFIIVVCSKGMKYFVDK 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               447 KNYKHKGG------GRGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDY 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                627 VRELP-SOGCLVVDVCV----SEEESRMAKLDPQLWPQRELVAHTLQSMVLPAEQV 677
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245 CFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPF-FSSCLND-----CLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SC-EGDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQ--HTRQGSRRNYFRSKSG
                                                         HVIADAQNITISQYACHDQVAVT-ILWS-PGALGIEFLKGFRVILEELKSEGRQCQQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       649 PALDGSAALQPLIHTVKAGSPSDMP--RDS-----GIYDSSV---PSSELSLPL----
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Patent No. 6072033
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             607 CKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQD------
                                                                                                                                                                                                                     D---LLLQPDNLACKPFWKPRNLNI----SQH----
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STREET: 51 University Street
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STATE: WA
COUNTRY: US.
ZIP: 98101
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US-09-022-255-2
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                                                                   -----SQHGG 640
                                                                                                                                                    618 VKRAPLVRE-PGSQACLAIDPLVGEEGGAAVAKLEPHIQPRGQPAPQPLHTLVLAAEEGA 676
  502 CYFSEVSCDGDVPDLFGAAPRYPLMDRFEEV--YFRIQDLEMFQPGRMHRVGELSGDNYL 559
                                         549 RSKSGRSLYVAICNMHQFIDEEPDWFE-----KQFVPFHPPPLRYREPVLEKFDSGL 600
                                                                                                                                                                                                   LDQDGEARPALDGSA---ALQ----PLLHTVKAGSPSDMPRDSGIYDSSVPSSELSLP 691
                                                                                                                                                                                                                                          677 LVAAVEPGPLADGAAVRLALAGEGEACPLLGSPGAG-----RNSVLF---LPVDPEDSP 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40 GWRM------KAAARPRL-----CVANEGVGPASRNSGLYNITFKYDNCTTYLNPVGK 86
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                                                                                                                                                                                                                                                                                 740
                                                                                                                                                                                                                                                                                                                      L--GSSTPMASPDLLPEDVR-----EHLEGLMLSLFEQSLSCQAQGGC 768
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08620694A

Patent No. 586286
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
NUMBER OF SEQUENCES:
ADDRESSEE: Immunex Corporation
                                                                                                                                                                                                                                                                                 LMEGLSTDQTETSSLTESVSSSSGLGEERPPALPSKLLSSGSCKADLGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 98101
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
                                                                                                                     601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USSN 08/538,765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/620,694A
FILING DATE: 21 MARCH 1996
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/538
FILING DATE: 7 AUGUST 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410
FILING DATE: 23 MARCH 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET UNBER: 26,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-08-620-694A-2
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510 ICSERDVPDLFNITSRYPLMDRFEEV--YFRIQDLEMFEPGRAHHVRELTGDNYLQSPSG 567
                                                                           554 RSLYVAICNMHQFIDEEPDWFEKQFVPFHP----PPLR---YREPVLEKFDSGLVLNDVM 606
                                                                                                            627 VRELP-SDGCLVVDVCV----SEEESRMAKLDPQLWPQRELVAHTLQSMVLPAEQV 677
                                                                                                                                                                                                                                                                                                                 -----ALPSKLLSSGSCKADLG 739
                                                                                                                                                                                                                                                                                                                                                                                                            649 PALDGSAALQPLLHTVKAGSPSDMP--RDS-----GIYDSSV---PSSELSLPL----
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7.6%; Score 306; DB 3; Length 864;
Best Local Similarity 22.5%; Pred. No. 1.6e-22;
Matches 189; Conservative 129; Mismatches 320; Indels 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09022696

Patent No. 6072037

GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TIPLE OF INVENTION, No. 6072037el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,696
                                                                                                                                                                                607 CKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQD--
                                                                                                                                                                                                                                                                                                                                                                                  693 ----MEGLSTDQTETSSLTESVSSSGLGEEEPP-
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51 University Street
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 261
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08
FILING DATE: 23 MARCH 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NO NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS: ADDRESS: Immunex C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (206)
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TELEFAX: (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             447 KNYKHKGG------GRGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDY 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         455 AKWKAILGWAEPAVQLRCDHWKPAGDLFTAAMNMILPDFKR-----PACFGTYVVCYFSG 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          497 SC-EGDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQ--HTRQGSRRNYFRSKSG 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87 HVIADAQNITISQYACHDQVAVT-ILWS-PGALGIEFLKGFRVILEELKSEGRQCQQ--- 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --LILKDPKQLNSSFKRTGMESQPFLNMKFETDYFVKVVPPPSIKNESNYHPFFFRTRAC 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132 LSMLQHHRKRWRFSF-----SHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKIIFVPDC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200 D---LILLQPDNLACKPFWKPRNLNI----SQH---------GSDMQV 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 EDSKOKOMITISCVSSGSLWDP-NITVETLDIQHLRVDFTLWNESTPYQVLLESFSDSENHS 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231 SFD------HAPHNFGFRFFYLHYKLKHE---GPFKRKTCKQEQTTETTSCLL 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     245 CFDVVKQIFAPRQEBFHQRANVTFTLSKFHWCCHHHVQVQPF-FSSCLND-----CLR 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         275 QNVSPGDYIIELVDDTNTTRKVMHYALKPV--HSP-WA-GPIRAVAITVPLVVISAFATL 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             331 FTVMCRKKQQENIYSHLDEESSESSTYTAALPRERLRPRFKVFLCYSSKDGQNHMNVVQC 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             391 FAYFLODFCGCEVALDLWEDFSLCREGOREWVIOK----IHESOFIIVVCSKGMKYFVDK 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40 GWRM------KAAARPRL-----CVANEGVGPASRNSGLYNITFKYDNCTTYLNPVGK 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tch 7.6%; Score 306; DB 3; Length 864; al Similarity 22.5%; Pred. No. 1.6e-22; 189; Conservative 129; Mismatches 320; Indels 202;
          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/620,694
FILING DATE: 21 MARCH 1996
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
FILING DATE: 7 AUGUST 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
ATTONNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / MOLECULE TYPE: protein US-09-022-255-2
                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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Best Local
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42;

GWRMKAAARPRLCVANEGVGPASRNSGLYNITFKYDNCTTYLNPVGK 86 :	HVIADAQNITISQYACHDQVAVT-ILMS-PGALGIEFLKGFRVILEELKSEGRQCQQ 141 ::	LILKDPRQLNSSFKRTGMESQPFLNMKFETDYFVKVVPFPSIKNESNYHPFFRTRAC 199 	DLLLQPDNLACKPFWKPRNLNISQHGSDMQV 230 : : : : : : EDSKWKWTTSCVSSGSLWDP-NITVETLDTQHLRVDFTLWNESTPYQVLLESFSDSENHS 244	SFDHAPHNFGFRFFYLHYKLKHBGPFKRKTCKQEQTTETTSCLL 274	QNVSPGDYIIELVDDTNTTRKVMHYALKPVHSP-WA-GPIRAVAITVPLVVISAFATL 330	FTVWCRKKQQENIYSHLDEESSESTYTAALPRERLRPRPKVFLCYSSKDGQNHMNVVQC 390 	FAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQKIHESQFIIVVCSKGWKYFVDK 446	KNYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDY 496 :	SC-EGDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFRSKSG 553	RSLYVAICNWHQFIDEBPDWFEKQFVPFHPPPLRYREPVLEKFDSGLVLNDVM 606 	CKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEAR 648 :	PALDGSAALQPLUHTVKAGSPSDMPRDSGIYDSSVPSSELSLPL 692 ::: ::	MEGLSTDQTETSSLTESVSSSGLGEEEPPALPSKLLSSGSCKADLG 739
	HVIADAQNITISQYACHDQ :: :: XINLSVSSTQHGEL	LILKDPKQLNSSFKRTG :: : - - LSMLQHHRKRWRFSF	DLLLQPDNLACKPFWK : : : : EDSKMKMTTSCVSSGSLWD		QNVSPGDYIIELVDDTNTT 	FTVMCRKKQQENIYSHLDE : : IICMTWRLSGADQEKHGDD			SC-EGDVPGILDLSTKYRL : :::: CSERDVPDLFNITSRYPL		CKPGPESDFCLKVEAAVLG : VRELP-SDGCLVVDVCV	PALDGSAALQPLLHTVKAG : :: PAAHVVEPLHLPDGSG	MEGLSTDQTETSSL :: :: : MSPDHLQGDAREQLESLML
40	87	142	200	231	275	331	391	447	497	554	607	649	693
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Search completed: August 9, 2005, 11:51:08 Job time : 42.7138 secs

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                Copyright
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OM protein - protein search, using sw model

August 9, 2005, 11:37:17; Search time 30.2019 Seconds (without alignments) 2398.896 Million cell updates/sec ü

US-10-717-282-2 4013 1 MAPWLQLCSVFFTVNACLNG.......CKADLGCRSYTDELHAVAPL 753 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No. Score Match No. Score Match 1 3005 74.9 2 126.5 3 126.5 4 117 2.9 4 117 2.9 9 115.5 110 2.7 116.5 110 2.7 110 2.7 110 100 2.7 110 2.7 110 2.7 110 2.7 110 2.7 110 2.7 110 2.7 110 2.7 110 2.7 110 2.7 110 2.7 110 2.7 110 2.7 110 2.7	þ				
100 100 100 100 110 110 110 110	Query Match	Length	DB	ID	Description
126.5 126.5 1117 1117 1117 1118.5 1118.5 1108.5 100	74.9	564	7	T42695	hypothetical prote
126.5 117 117 118.5 118.5 118.5 119.5 100.5 100.5 100.5 100.5 100.5 100.5 101.5 101.5	4.2	846	N	T27282	
117 117 117 118.5 110 110 100 100 100 100 100 100 100 10	3.2	718	N	T30113	
117 118.5 118.5 118.5 118.5 118.5 110.5 10	2.9	757	~	T09081	telomere-associate
117 118.5 118.5 118.5 110 100 100 100 100 100 100 100 100 10	2.9	917	~	T04661	
116.5 115.5 110 110 108.10 107.5 107.5 103.5 103.5 101.5 101.5	2.9	2946	~	T00867	
115.5 1110 1110 1100 1100 100.5 100.5 100.5 100.5 100.5 101.5 101.5 101.5 101.5	2.9	901	~	F83781	transposase (08) /
115 110 110 100 100 100 100 100 100 100	2.9	938	~	149071	protein kinase - m
110 108.15 107.5 107.5 107.5 103.5 103.5 103.5 101.5 101.5	2.9	966	~	S37627	protein-tyrosine k
108.5 108.5 107.5 107.5 106.5 106.5 103.5 103.5 101.5 101.5		535	7	T17212	hypothetical prote
108.5 107.5 106.5 106.5 106.5 103.5 103.5 101.5 101.5 101.5	2.7	592	7	149239	vesicle transport
107.5 106.07 106.07 106.5 103.5 103.5 101.5 101.5 101.5	2.7	3788	~	T13960	beige protein homo
106 106.5 106.5 105 103.5 101.5 101.5 101.5	2.7	3942	~	T42730	Bassoon protein -
106.5 106.5 108.5 103.5 103.5 101.5 101.5 101.5	2.7	3788	7	T30851	lysosomal traffick
106 105 103 103 103 103 101 101 101 101	2.7	638	~	D86477	protein F1504.27 [
105 105 103.5 103.5 102 101.5 101.5	2.6	1448	7	AI2007	Subtilase family p
105 103.04 103.5 1002 101.5 101.1	5.6	901	7	JC6093	dead ringer nuclea
104 103.5 103.5 1002 101.5 101.5	5.6	1571	7	T14155	zinc finger protei
103.5 103.5 102 101.5 101.5 101.101	5.6	1462	-	B36182	protein-tyrosine-p
103.5 102 101.5 101.5 101.1	5.6	663	7	A39897	GTPase-activating
102 101 101.5 101.5 101	5.6	930	~	A84668	Argonaute (AGO1)-1
102 101.5 101.5 101 101	2.5	813	~	B47485	ABR protein 2 - hu
101.5	2.5	859	0	A49307	98K GTPase-activat
101.5	2.5	822	~	A47485	ABR protein 1 - hu
101 101 101	2.5	1639	7	T50119	probable sensory t
101	2.5	641	7	T05497	hypothetical prote
101	2.5	664	~	T51247	ARR2 protein [impo
	2.5	1275	0	A38985	nucleotide exchang
10	2.5	938	7	T05533	hypothetical prote

Rho GTPase activat	hypothetical prote	serine/threonine p	Z13 protein - mous	gag-abl polyprotei	190 kd antigen pre	sex-determining re	hypothetical prote	hypothetical prote	type I site-specif	mouse developmenta	exodeoxyribonuclea	exodeoxyribonuclea	exodeoxyribonuclea	hypothetical prote	hypothetical prote
E59434	T24643	E96949	823069	FOMVGM	H71716	A31491	863059	T33782	AD2381	I48653	G86582	H72041	C81624	T16124	833794
0	N	cv.	N	-	N	~	~	N	N	7	~	~	~	~	7
974	1001	657	794	981	341	783	970	353	963	993	1050	1050	1050	526	820
2.5	2.5	2.5	2.5	2.5	2.5	2.5	2.5	2.5	2.5	2.5	2.5	2.5	2.5	2.4	2.4
100.5	100.5	99.5	99.5	99.5	66	66	66	98.5	98.5	98.5	98.5	98.5	98.5	98	98
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

		hypothetical protein DKFZp434N1928.1 - human (fragm	Charles Thomas Constitutions
		protein DK	000,000
RESULT 1	T42695	hypothetical	

C;Species: Homo sapiens (man)
C;Decies: Homo sapiens (man)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T42695
B;Bloecker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, submitted to the Protein Sequence Database, November 1999
A;Reference number: Z22230
A;Accession: T42695
A;Accession: T42695
A;Accuse: mRNA
A;Residues: 1-564 <AAA>
A;Cross-references: UNIPROT: Q9UFAO; EMBL: AL133097
A;Cross-references: adult testis; clone DKFZp434N1928
C;Genetics:
A;Note: DKFZp434N1928.1

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Gaps ö 74.9%; Score 3005; DB 2; Length 564; 99.8%; Pred. No. 1.9e-232; Artive 0; Mismatches 1; Indels Best Local Similarity 99.8 Matches 563; Conservative Query Match Best Local Similarity

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190 HPFFFRTRACDLLLQPDNIACKPFWKPRNLNISQHGSDMQVSFDHAPHNFGFRFFYLHYK 249 310 GPIRAVAITVPLVVISAFATLFTVMCRKKQQENIYSHLDEESSESSTYTAALPRERLRPR 369 QFIIVVCSKGMKYFVDKKOYYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKF 489 549 301 IAVYFDYSCEGDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFR 360 SKSGRSLYVAICNWHQFIDEEPDWFEKQFVPFHPPPLRYREPVLEKFDSGLVLNDVMCKP 609 361 SKSGRSLYVALCNMHQPIDEEPDWFEKQFVPFHPPPLRYREPVLEKFDSGLVLNDVMCKP 420 GPESDFCLKVEAAVLGATGPADSQHESQHGCLDQDGEARPALDGSAALQPLLHTVKAGSP 669 429 | HEFFERTRACDILLOPDNIACKFFWKPRNLNISQHGSDMQVSFDHAPHNFGFRFFYLHYK PKVFLCYSSKDGQNHMIVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQKIHES IAVYFDYSCEGDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFR 121 370 181 430 490 550 610 셤 ò 요 ò ద ò 셤 8 ద à 엄 à 임 ò ò

Page 2

д	421 GPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAALQPLLHTVKAGSP 480	qa	704 DELKEKFAAKRDLEVEVLDSEDVKLLEDVKCAPGPIHVEPTEPEVLEPAEEPMEE 758
% a	670 SDWPRDSGIYDSSVPSSELSLPIMEGLSTDQTETSSLTESVSSSSGLGEEEPPALPSKLL 729 	<i>≿</i> 8	637 QHGGLDQDGBARPALDGSAALQPIL-HTVKAGSPSDMPRDSGIYDSS-VPSSELS 689 11
Qy Db	730 SSGSCKADLGCRSYTDELHAVAPL 753	RESULT 3 T30113 hypotheti C;Species C;Date: 1	RESULT 3 T30113 hypothetical protein F56D1.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #text change 09-Jul-2004
T27282 hypothetical C;Species: C; C;Date: 15-OC C;Accession:	T27282. T27282. Mypothetical protein Y64G10A.e - Caenorhabditis elegans C,Species: Caenorhabditis elegans C,Species: L5-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 D.Aircesalon: T27282	C, Accession R, Chissoe, submitted to A, Description A, Accession	C;Accession: T30113 R;Chissoe, S.; Wilson, R. Stibhitsed to the EMBL Data Library, November 1995 A;Description: The sequence of C. elegans cosmid F56D1. A;Reference number: Z20737
Submit A;Refe A;Accel A;Stati	Submitted to the EMBL Data Library, September 1999 A;Reference number: 220336 A;Accession: T27282 A;Status: preliminary; translated from GB/EMBL/DDBJ	A;Status: A;Molecul A;Residue A;Cross-I	preliminary; translated from GB/EMBL/DDBJ e type: DNA s: 1-718 <chi> eferences: UNIPROT:Q10128; EMBL:U39997; PIDN:AAA81100.1; CESP:F56D1.2</chi>
A, Resi	tues: 1-846 <wll> s-references: UNIPROT: Q9NA64; EMBL: AL110498; PIDN: CAB54470.1; CESP: Y64G10A.e imental source: clone Y64G10A</wll>	A;Gene: C A;Introns C;Superfa	A;Gene: CESP:FS6D1.2 A;Introns: 93/1; 121/2; 163/3; 459/1; 517/3; 555/1; 615/3; 667/3 C;Superfamily: Caenorhabditis elegans hypothetical protein FS6D1.2
C;Gene A;Gene A;Intr C;Supe	. 1568. 2088: Y64G10A.e 208: 106/1; 198/3; 261/1; 301/3; 386/1; 416/2; 475/1; 510/3; 580/2; 815/3 26mily: Caenorhabditis elegans hypothetical protein Y64G10A.e	Query Match Best Local Matches 8	atch 3.2%; Score 126.5; DB 2; Length 718; cal Similarity 20.6%; Pred. No. 0.1; B9; Conservative 68; Mismatches 165; Indels 111; Gaps 20;
Query M Best Lo Matches	Query Match Best Local Similarity 21.4%; Pred. No. 3.9e-05; Matches 141; Conservative 82; Mismatches 225; Indels 211; Gaps 37;	상 옵	315 VAITVPLVVISAFATLFTVMCRKKQQENIYSHLDEESSESSTYTAALPRERLRP 368
& 8	99 QYACHDQVAVTILWSPGALGIEFLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFKRTG 158	දි දි	369 RPKVFLCYSSKDGONHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIOKIHE 428
ري م	159 MESQPFLNNKFETDYFVKVVPFPSIKNESNYHPFFRTRACDLLLQPDNLAC-KPFWKRR 217	දුරු පු	429 SQFIIVVCSKGMKYFVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQSSSAALSK 488 1
oy Oy	218 NINISQHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFRKRTCKQEQTTETTSCLLQNV 277 1:	ò a	489 FIAVYEDVSCEGDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTRQGSRR 545 : : : : : : : :
දු දු	278 SPGDYIIELVDDTNTTRKVMH-YALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVM 334 416	À q	546 NYFRSKSGRSLYVALCNMHQFIDEREDWFEKQFVPFHPPPLRYREPVLEKF 596 576 NVTQNISEAQIHEMNLCASRMMSFFVRNBNWLETRWKPKDELAALHLKRQSPVIVPI 632
දු දු	335 CRKKQQENIYSHLDEESSESSTYTAALPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAYF 394 :	<i>ò</i> 9	597 DSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAA 656 :
oy Oy	395 LQDFCGCEVALDLWEDFSLCREGQREWVIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGG 454 :	රු සි	657 LQPLIHTVKAGSPSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTFTSSLTESVSSSS 714 664 LQPHASHQNQPLILLPPEQCGPDSDSDSESDSSSESESESDNB 706
& Q	455 GRGSGKGELFLVAVSAIAEKURQAKQSSSAALSKFIAVYFDYSCEGDVPGILDLSTKY 512 :	λό G	715 GLGEERPPALPSK 727
\$ g	513RLMD-NLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAI 560	RESULT 4 T09081	RESULT 4 T09081 Talomoreseconisted recollike helicase - smut funcus (Ustilaco mavdis) (fragment)
yo O	561 CNMHQFIDEEPDMFEK	C;Species C;Date: 1 C;Accessi	Cispecies: Ustilago maydis (corn smtt) Cispecies: Ustilago maydis (corn smtt) Cipaces: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004 CiAccession: 1709081
ð	590 EPVLEKFDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHES 636 :: : :	Risanchez Genetics A;Title:	Ribanchez-Mionbov, F., Gudman, F., Genetics 148, 1043-1054, 1998 A;Title: Organization of chromosome ends in Ustilago maydis: recQ-like helicase motifs a

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105

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145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              572 IYIYSLAHVVQGVKKVLHKKKFSSSPICSASTFYGTSGVG---LTLVFTDGTVEIRSLPE 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SM----NRVYKKDNSVCHEGIITSSSPREKKSMFGSVFKTKSKRTTDTEPESSKETIEEL 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             381 GONHMAVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQKIHESQFIIVVCS--- 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GK-------QDTSG------NGPDTSRES----TVEEISIRQPSVLVCSEKA 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----KGMKYFVDKKNYKHKG------GGRGSGKGELFLVAVSAIAE----K 474
                                                                                                                                                                                                                                                                                              106 VAVTILWSPGALGI--EFLKGFRVILBELKSEGROCOQLILKDPKOLNSSFKRTGMESOP 163
                                                                                                                                                                                                                                                                                                                                                                                       --FLUMKRETDY-----FVKVVPFPSIKNESN---YHPFF-----FRTRACDLLLQPD 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     266 SHILINISDE-DYAQLAKDAVPFLPFHTVPKESSRSAHFPGFTKVRNVYITGHCDGTISVW 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      385 LTENSFIPFQGSLKKGNNHIVQSVKYIKLTGSITCIQKSQNSKHLAIGSDQGHDSLVEVI 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DDINITRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFT------- 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   517 NLPQLCSHLHSRDHGLQEPGQHTRQGSRR-----NYFRSKSGRSLYVALCNMHQFIDEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  483 FESCIVQGFEKNVLVVAMRDSSVFA-LDSDTGNMIGTNMIKPK-----KPFKVLYMQILD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSOLKOTSIRGFTYSSPKPNSLPEITISASWDGDLVMVNGDDELIVSSVLPQKETFRLVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DODGEARPALDGSAALQPLLHTVKAGSPSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  475 IRQAKQS-----SSAALSKFIAVYFDYSCEGD------VPGILDLSTKYRLMD
                                                                                                                                                                                                                  NGSRVSV-----GYSNG-DILIWSIPSKGECSPESSAMICKLNLGYKSEKIPIASLKWVY
                                                                                                                                                                                                                                                                 --GPASR-----NSGLYNITFKYDNCTTYLNPVGKHV---IADAONI--TISQYACHDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NLACK----PFWKPR-NLNISQHG-----SDMQVSFDHAPHNFGFRFFYLHY
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                                                                                                                    320;
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A;Note: F8D20.70
C;Superfamily: Arabidopsis thaliana hypothetical protein F8D20.70
                                                                     Length 917;
                                                                     Query Match 2.9%; Score 117; DB 2; Length 91°
Best Local Similarity 18.3%; Pred. No. 0.84;
Matches 167; Conservative 130; Mismatches 296; Indels
                                                                                                                                                                   NGSQLAVAAGGSGRARGADTCGWRM--KAAARPR----LCVANEGV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                571 PDWFEKQFVPF--------
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Appr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T04661
R;Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Jesse, T.; Heijnen, L.; Vos, P.; Mewes, submitted to the Protein Sequence Database, July 1998
A;Recession: T04661
A;Accession: T04661
A;Accession: T04661
A;Recession: T04661
A;Rescrimental source: cultivar Columbia; BAC clone F8D20
C;Genetics: A
A;Rep Position: 4
A;Introns: 13/3; 58/2; 93/1; 274/3; 333/3; 335/1; 437/3; 536/1; 624/2; 665/3; 685
                                                                                                                                                                                                                                                                                                                       27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        412 SLCREGOREWVIOXIHESQFIIVVCSKGMKYFVDK------KNYKHKGGGRGS----- 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----RLMDNLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFRS 550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             551 KSGRSLYVAICNMHQFIDEEPDWFEKQFVPFHPPPLRYREPVLEKFDSGLVLNDVMCKPG 610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         611 PESDPCLKVEAAVLGATGPADSQH---ESQHGGLDQDGEARPALDGSAALQPLLHTVKAG 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        420 PGHHF-----QARGPGDQFHFTAPAQAGDPSTQGSRHPSMHGSS--HPSMH----- 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPSDMPRDSGIYDSSVPSSE-LSLPLMEGLSTDQTETSSLTESVSSS----SGLGEEEPPA 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----GSSHPSSHGSSHPSIHGSSHPSIHGSS-HPSIHGSGQHGGQRRKQQPD 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------VVISAFATLFTVMCRKKQQENIYSHLDEESSESSTYTAALP----- 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --RERLRPRPKVF-----LCYSSKDGQNHMNVVQCF-AYFLQDFCGCEVALDLWEDF 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----NGORD------RIIVYCTS--KELVARLAEMLGCAAYSSESGSEADKAAIIQ 290
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A;Reference number: Z16557; MUID:98198830; PMID:9539423
A;Accession: T09081
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-757 ASAN>
A;Cross-references: UNIPROT:013399; EMBL:AF030885; NID:92642221; PID:92642222
A;Experimental source: strain FB2
C;Genetics: UTASrecQ
C;Keywords: DNA binding
                                                                                                                                                                                                                                                                                                                                                                    268 ETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAV----AITVPL-- 321
                                                                                                                                                                                                                                                                                                                                                                                                                ETTILILPTVALRANMLAKLDVMN----IRYHVWQP-GSKKAAPIVLVSTBAAITLAFKE 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----GKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGIL--DLSTKY
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                       56; Mismatches 187; Indels 190;
                                                                                                                                                                                                                                                                        Score 117; DB 2; Length 757;
Pred. No. 0.63;
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 20.4%;
Matches 111; Conservative 5
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hypothetical protein At2g45540 [imported] - Arabidopsis thaliana N;Alternate names: hypothetical protein F17K2.7 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004 C;Accession: T00867; G84891 R;Rounsley, S.D.; Kaul, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMR. Data Library March 1948	QY 442YGYUKKANYKHKGGGRGSGKGELFLVAVSAIAEKLROAKQSSSAA- 485 B37 QLLLDGCRRCYWMISEKDSETTFPLDGNTRQWGELNALIDELLVIIELLMGAASPSLAAD 896 QY 486 -LSKRIAVYFDYSCEGDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQH 538 B97 DLRRLGGFIIDSPQPNQVARVIHLMYRLVVQPNAARAQMFAEVFITSGGIETLLVLQRE 956
co cne Emble Data Library, Lion: Arabidopsis thaliana se number: Z14207 nn: T00867	Qy 539 TRQGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFEKQFVPFHPPPLRYREPVLEKFDS 598 :
A;Status: translated from Gb/EmbL/DDbJ A;Molecule type: DNA A;Residues: 1-2346 <rou> A;Cross-references: UNIPROT:064634; EMBL:AC003680; NID:g2979540; PID:g2979554</rou>	Qy 599 GLVLNDV-MCKPGPESDFCLKVEAAVLGATG-PADSQHESQHGGLDQDGEARPALDGSAA 656
A; Experimental source: cultivar Columbia R;Lin, X; Kaul, S.; Rounaley, S.D.; Shear, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J	Qy 657 LQPLLHTVKAGSPSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSGL 716
naliana.	Oy 717 GEEEPPALPSKLLSSGSCKADLGCRS 742 : Db 1075 NNVYNVDNSDAVVVGIIRLIGALISSGHLTFDFDARS 1111
DNA ⁻ 46 <sto> 88: GBAE002093; NID:G2979554; PIDN:AAC06163.1; GSPDB:GN00139</sto>	RESULT 7 F83781 FRANSPORSE (08) / ABC transporter (ATP-binding protein) BH1054 [imported] - Bacillus hal
A; Gene: Films; Atzgabs40 A; Maption: 5 A; Introns: 652/1; 913/3; 1165/3; 1210/3; 1245/3; 1283/3; 1309/2; 1336/3; 1438/3; 1638/2; ; 2449/2; 2481/3; 2643/1; 2890/3; 2931/3	C.) Species: Davillus mardourans C.) Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004 C.) Accession: F83781 R.) Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran
Query Match 2.9%; Score 117; DB 2; Length 2946; Best Local Similarity 18.7%; Pred. No. 4.8; Matches 164; Conservative 105; Mismatches 314; Indels 294; Gaps 40;	Nuclear Acids Res. 28, 4317-4331, 2000 A,Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and c. A,Reference number: A83650, MUID:20512582, PMID:11058132 A,Accession: F83781
OY 2 APWLQLCSVFFTVNACLNGSQLAVAAGGSGRARGADTCGWRWKAAARPRLCVANEGVGPA 61 DD 393 ATWIYIESFADTLNAATAAAAIAAAAAAKSGKTSAMSAAAAASALAGEG 441	A, Status: preliminary A, Mole type: DNA A, Rosidues: 1-901 <5TO> A, Residues: 1-901 <5TO> A, Cross-references: UNIPROT: Q9KE04; GB: AP001510; GB: BA000004; NID: 910173440; PIDN: BAB0477
OY 62 SRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVTILWSPGALGIEF 121 :	A;bxperimental source: strain C-125 C;Genetics: A;Gene: BH1054
122 LKGFRVILEELKSEGRQCQLILKDPKQLNSSFKRTG	Query Match 2.9%; Score 116.5; DB 2; Length 901; Best Local Similarity 19.6%; Pred. No. 0.9; Matches 112; Conservative 76; Mismatches 169; Indels 215; Gaps 27;
159 MESQPFLNMKFETDYFVKVVPFPSIKNESNYHPFFFRTRACDLL	Qy 61 ASRNSGLYNITPKYDNCTTYLNPVGKHVIADAQNITISQY-ACHDQVAVTILWSPGALGI 119
DB 523 IESKEFITTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	Qy 120 BFLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFKRTGMESQPFLMMKF 169 120
261 CKQEQTTETTSVMHYA	
301 LKPVHSPWAGPIRAVAITVPLVVISAFALLFTVM	Qy 218 NLNISQHGSDMQVSFDHAPHNFGFRFYLHYKLKHBGPFKRKTCKQBQTTET 269
335CRKKQQENIYSHLDEESSESSTYTAALPRERLRPRPKVFLCYSSKDGQN	Qy 270 TSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVIS-AFA 328 2
DB 730 HPGNNEELCRIQGPEILARILSYLLHSLABLDRKHDGVGEEEL-VAAIVSLCQSQR1N 786 QY 384 HMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQXIHESQFIIVVCSKGMK 441	329 TLFTVMCRKKQQENIYSHLDEESSESSTYTAALPRERLRPRPKVFLCYSSKDGQNHMMVV
_	Qy 389 QCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQKIHESQFIIVVCSKGMK 441

	qy 613 SDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAALQPLHTVKAGSPSDM 672	45; 52 229 93 287 144	
	(fragment) (house mouse) quence_revision 02-Jul-1996 #text_cham L.; Robertson, E.J. 1994 of novel protein kinases expressed in 071; MUID:95200798; PMID:7893599 cranslated from GB/EMBL/DDBJ ryosine kinase, receptor type eph; file mbrane protein chanse ATP-binding motif 0melogy <sam> 2.9%; Score 115.5; DB 2; Length</sam>	5; TCGW TCGW C	145 KDEKQLINSEKRTGMESQPFLUMKFETDYEVKVVPPPSIKNESNYHPFFFRTRACDLLLQ 1338 FVPRQLGLTERRVHISHLAHTRYTPEVQAVIGYSGKSPLPPRYAAVNITTNQAA 205 PDNLACKPFWKPRNLNISQHGSDMQVSFDHAPHPGFRFFYLHYKLKHGGPF-KRKTCKQ 193 PSEVPTLHSHSTGGSSLTLSWAPPERFNGVILDYEWKYFEKSKAIAS 264 EQTTETTSCLLQNVSP-GDYIIELVDDTNTTRKV

9	RESULT 11 149239 vesicle tra	C,Species: C,Date: 02- C,Accessior R,Tellam, C	J. Biol. Ch A;Title: Mo A;Reference A;Accession	A;Status: I A;Molecule A;Residues: A;Cross-ref	C,Genetics: A,Gene: mur	Query mar Best Loca Matches	3	e da 8	qu	δ	qa —	Š	q ₀	λο	q a	<i>\</i> 0	q ₀	200	දුරු 	\doldo	•	, ,	dd crampad	T13960 T13960 Deige prote C;Species:	C, Date: 20-C, Accession R, Mori, M.;
346 HLDEESSESTYTAALPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAYFLQDFC-GCEVA 404 	405 LDLWEDFSLCREGQREWVIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGGRGSGKGELF 464	465 LVAVSAIAEKIRQAKQSSSAALSKFIAVYFDYSCEGDVPGILDLSTKYR 513 : : : 662 -VAIKTLKVGYTERQRRDFLSEASIMGQFDHPNIIRLEGVVTKSRPVMI 709	LMDNLPQLCSHLHSRDHGLQEPGQHTRQGSRRNY-FRSKSGR 	555 SLYVAICNWHQFIDEEPDWFEKQFVPFHPPPLRYREPVLEKFD 597 ::	SGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGBARPA	817 SASDVWSYGIVMWEVMS	861 MDCPTALHQLMLDCWVRDRNLRPKFSQIVNTLDKLIRNAASLKVIASAQSGMSQPLLDRT 920	697 STDQTETSSLTESVSSSGLGEEEPPALPSKLLSSGSCKADLGCRSYTDEL 747			agments)	as a treat cualige	R;Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, September 1999	: IIIIDEI: 418/23	Scatus: preliminary Molecule type: mRNA Molecule type: mRNA	1-488;489-535 <fou> rences: UNIPROT:Q9NTU6; I</fou>	ical source: adult testis; clone Darages#fall : cDNA sequence contains a -1 frameshift near codon 488	DKF2p434P211.1	Match 2.7%; Score 110; DB 2; Length 535;	Fred. NO. 1 12; Mismatch		103 RYNQTSQTSWTSSCTNRNAISSSYSSTGGLPGLKRRRGPASSHCQLTLSSSKTVSEDRPQ 162	521 LCSHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFEKQF 578 :	579 VPFH-PPPLRYREPVLEKFDSGLVLNDVMCKPGPESDFCLKVEAA 622	VLGATG-PADSQHESQHGGLDQDGEARPALDGSAALQPLLHTVKAGSPSDMP
ζλ Ob	oy Ob	Qy Db	oy B	Qy Db	ે હ	g &	qo	ζ Dp		RESULT 10 T17212	hypothetic C,Species:	C; Accessic	R;Poustka, submitted	A; Accessic	A; Molecule	A; Keslaues: A; Cross-refe	A; Note: the	A;Note: DF	Query Ma	Matches	ογ	අු	Qy Db	<u>ک</u> م	۲۵ ز

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on: 149239
J.T.; McIntosh, S.; James, D.E.
Them. 270, 5857-5863, 1995
Alecular identification of two novel Munc-18 isoforms expressed in non-neuronal ce number: 149238; MUID:95197608; PMID:7890715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ferences: UNIPROT:Q60770; EMBL:U19521; NID:g642027; PIDN:AAA69913.1; PID:g64202
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0-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
on: T1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
on: T1996
to Nishikawa, T.; Higuchi, K.; Nishimura, M.
to the EMBL Data Library, November 1998
tion: Deletion in the beige gene of the beige rat due to recombination between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22;
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-----KATEGKTSLSALTQLMKKOMPHFRKQISKQVV----HL 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   527 SRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNWHQFIDEEPDWFEKQFVPFHPPPL 586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       621 AAVLGATGPADSQHESQHGGLDQDGEARPALDGSAALQPLLHTVKAGSPSDMPRD-SGIY 679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  403 -VALDLWEDFSLC-----REGOREWVIQKIHESQFIIVVC-----SKGMKY----- 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | | | : : | | : : | | : : | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 205 SKIAQLVEKKIEDYYKIDEKGLIKGKTQSQLLIIDRGFDPVSTVIHEL------ 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     321 LVVISAFATLFTVMCRKKQQ------ENIYSHLDEESSESSTYTAALPRERLRPRPK 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 IMLLDEFTTKLLSSCCKMTDLLEEGITVIENIYKNREPVRQMKALYF-----ISPTPK 86
676 SG-IYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSGLGEEFPPALPSKLLSSG 732
                                                                                                            ----PAPFPAASMDAG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tch 2.7%; Score 110; DB 2; Length 592; al Similarity 18.5%; Pred. No. 1.6; 93; Conservative 64; Mismatches 157; Indels 188; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             372 VFLCYSSKDGONHMNVVQCFAYFLQDFC-------GCE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   preliminary; translated from GB/EMBL/DDBJ type: mRNA
                                                                                 322 PGPLFSSSDP----LPATSSDSQDSAQVTSLI---
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C; Keywords: alternative splicing
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Best Local Similarity 19.1%;
Matches 58; Conservative
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A,Reference number: 217837
A,Accession: T13960
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,FOlecule type: mRNA
A,Residuse: 1-3788 + MORA
A,Cross-references: UNIPROT:09ZXX9; EMBL:AB020019; NID:d1241953; PID:d1035670; PIDN:BAA3
A,Experimental source: strain DA; spleen
A;Gene: beige
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                                                                                                                                                                                                                                                                                                                                                                                                                                            230 VSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTETTSCLLQNVSPGDYIIELVDD 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----GPSLHK----QASTDSPCSLRK----FYASLRDT 880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   290 INTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQQENIYSHLDE 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      881 DPKKRKTVHQ------DAHINTINLELCVAF-----LCVSKEADSDRRSAN- 920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESSESSTY--TAALPRERLRPREVVFLCYSSKDGONHMNVV----QCFAYFLQDFCGCEV 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALDLWEDFSLCREGOREWV--IQXIHESQFI----IVVCSKGMKYFVDKKNYKHKGGGRG 457
                                                                                                                                                                                                                                        551 GETLQGTLCGAGPSCGLPSPSYRF------OGILP---SSGSEDFLWKWDALEA 695
                                                                                                                                                                                                                                                                                       YONFIEGE--DRLHNTGIASHICNLIQKGNVIVQW------KLYNYIFNPVLQRGV 743
                                                                                                                                                                                                                                                                                                                                                         744 ELVHHCQQLSI-----TSAQTHMSSQLKQYLPQBVLQIYLKTLPILLKSRVIRDLFL 795
                                                                                                                                                                                                                                                                                                                                                                                     SIKN-----ESNY------HPF-FFRTRACDLILLQPDNLACKPFWKPRNLNISQHGSDMQ 229
                                                                                                                                                                                                                                                                                                                               -----FP 181
                                                                                                                                                                                                          GSQLAVAAGGSGRARGADTCGWRMKAAARPRLCVANEGVGPASRNSGLYNITFKYDNCTT 79
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C;Species: Mus musculus (house mouse)
C;Date: 11-Jan.2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T42730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     458 SGKGELF-----LVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILD----
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                                                                                                                                                                                                                                                                    YLNPVGKHVIADAQNITISQYACH--DQVAVTILWSPGALGIEFLKGFRVILEELKSEG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         921 ESEDTSGYDSTASEPLSHMLPRLSL------ENVVLPSPECLHH-----
                                                                                                                                                                                 98; Mismatches 267; Indels 235;
                                                                                                                                                   Length 3788;
                                                                                                                                                                                                                                                                                                                              ---RQCQQLILKDPKQLNSSFKRTGMESQPFLNMKFET-DYFVKVVP--
                                                                                                                                                      DB 2;
                                                                                                                                                       Score 108.5;
Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               543 SRRNYFRSKSGRSLYVAICNMHQFIDEEP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELPEAEGFSGSIVPNNLLESLTHG 1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                647 ARPALDG-SAALQP--LLHTVKAG 667
                                                                                                                                                       2.7%;
                                                                                                                                                                                   Conservative
                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             853 V-----
                                                                                                                                                      Query Match
Best Local Simil
Matches 144; (
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A;Description: may be involved in cytomatrix organization at the site of neurotransmitte A;Note: component of the presynaptic cytoskeleton C;Keywords: coiled coil; zinc finger
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A;Experimental source: strain C57BL/6J
R;Dieck, S.; Sanmarti-Vila, L.; Langnaese, K.; Richter, K.; Kindler, S.; Soyke, A.; Wex, J. Cell Biol. 142, 499-509, 1998
A;Title: Bassoon, a novel zinc-finger CAG/Glutamine-repeat protein selectively localized A;Reference number: Z22249; MUID:98345363; PMID:9679147
                                                                                                                                                                                                                      A;Residues: 1-3942 <DIE>
A;Cross-references: UNIPROT:088737; EMBL:Y17034; NID:g3413809; PIDN:CAA76598.1; PID:g341
A;Experimental source: strain 129 SVJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
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3692 PQASPAPAMQKKGQPGYPSSADYSQSSRAPSAYHHASESKKGSRQAHTGPSALQPKADTQ 3751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | | | | | | : : : | | : : : | | : | 3535 DICPQFCS----SHSMPDVQEHVKDGPRAHAYKREEGYMLDDSHCVVSDSEAYHLGQEE 3589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3644 PGRH------TSAKEHRHHSDHGRHSGRHAGEEPGRRAAKPHARDMGRHEARPH 3691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    610
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                                                                                                                                                                                                                                                                                                                                                      A;Map position: 9F1
A;Introns: 72/2; 208/3; 505/3; 675/3; 2889/3; 3582/1; 3851/3; 3886/1; 3930/1
A;Note: bassoon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lysosomal trafficking regulator, long splice form - mouse
N;Alternate names: beige protein homolog
C;Species: Mus muscallus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30851
R;Barbosa, M.D.F.S; Tchernev, V.T.; Kingsmore, S.F.
submitted to the EMBL Data Library, September 1996
A;Description: Two bg or not two bg? Longest isoform of mouse Lyst (beige) g
A;Reference number: 220903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAIC-----NMHQFIDEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -- PVLEKF------DSGLVLNDVMCKPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3590 TDWFDK---PRDARSDRFRHIGGHTVSSSOKRGPARHSYHDYDEPPEEGLWPHD---EGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PESDFCLKVEAAVLGATGPADSQHESQHG-----GLDQDG-------EARP-
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2.7%; Score 107; DB 2; Length 3788;
Best Local Similarity 19.5%; Pred. No. 44;
Matches 156; Conservative 104; Mismatches 288; Indels 254;
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-3788 <BAR>
                                                                                                                                      A;Accession: T42730
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.7%; Score 107.5;
19.1%; Pred. No. 43;
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PIDN: AAF79353.1; GSPDB:GN(

A, Reference number: A86141; MUID:21016719; PMID:11130712
A,Accession: D86477
A,Status: preliminary
A,Molecule tune

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1012 QGEMSRNENQELIRIS------1048
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                                                YLNPVGKHVIADAQNITISQYACH--DQVAVTILWSPGALGIEFLKGFRVILEELKSEG- 136
                                                                                                                                                                                                                                                                                                                                                                                      744 ELVHHCQQLSIPS-----AQTHMCSQLKQYLPQEVLQIYLKTLPVLLKSRVIRDLFL 795
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                                                                                                                                                                                                                         YOSFVFOE--DRLHNIQIANHICNLLOKGNVVVQW-------KLYNYIFNPVLORGV 743
                                                                                                                                                                                                                                                                                                          ---RQCQQLILKDPKQLNSSFKRTGMESQPFLNMKFET-DYFVKVVP-----FP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCNGVNHIIBLNYLDGIRSHSLKAFETLIVSLGEQQKDAAVLDV---DGLDİQQELPSLS 852
GSQLAVAAGGSGRARGADTCGWRMKAAARPRLCVANEGVGPASRNSGLYNITFKYDNCTT
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protein F1SO4.27 [imported] - Arabidopsis thaliana protein F1SO4.27 [imported] - Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: O2-Mar-2001 #text_change 09-Jul-2004
C;Accession: D86477
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H., Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
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2005, 11:49:54

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Search completed: August Job time: 35.2019 secs

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                                                                                                                                       153;
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A; Molecule type: DNA
A; Residues: 1-638 <STO>
A; Cross-references: UNIPROT: Q9LQF8; GB: AE005172; NID: g8778345;
C; Genetics:
A; Gene: F1504.27
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19.4%; Pred. No. 3.4;
7ative 63; Mismatches 175;
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(c) 1993 - 2005 Compugen Ltd.
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Q8HXE8
117R_HUMAN
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ALIGNMENTS

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                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Gilbert J.M., Gorman D.M.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF458067; AAM77571.1; -.
GO; GO:0016020; C:membrane; IEA
GO; GO:0004888; F:transmembrane receptor activity; IEA.
ENTERPROOIST TIR.
SEQUENCE 739 AA; 82440 MW; 1670803DDOCDOF17 CRC64;
                                                                         Last sequence update)
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Best Local Similarity 98.0°
Matches 738; Conservative
PRELIMINARY;
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LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQOENIYSHLDEESSESSTYTAA 360
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FLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFKRTGMESQPFLNMKFETDYFVKVVPF 166
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                                          PSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKPRNLNISQHGSDMQVSFDHAPHNFG
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PubMed=12958313; DOI=10.1074/jbc.M306936200;
Xiong S., Zhao Q., Rong Z., Huang G., Huang Y., Chen P., Zhang S.,
Liu L., Chang Z.;
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Catarrhini; Hominidae; Homo.
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Xiong S.Q., Huang G.R., Zhao Q.H., Chen P.L., Rong Z.L., Ye lend Y., Liu L., Pu X.Y., Chang Z.J.;

Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AF494208; AAM74077.1;

Genew, HGKC.117616; ILITRD.

GO; GO:0016020; Cimembrane; IEA.

GO; GO:0016020; Cimembrane; IEA.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Interleukin 17 receptor-like protein long form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liu L., Chang Z.;
"hSef inhibits PC-12 cell differentiation by interf
mitogen-activated protein kinase MAPK signaling.";
J. Biol. Chem. 278:50273-50282(2003).
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
MCBI_TaxID=9606;
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Altuvia Y., Ron D.;
"Alternative splicing generates an isoform of the human Sef gene with alternative splicing generates an isoform of the human Sef gene with altered subcellular localization and specificity.";
Proc. Natl. Acad. Sci. U.S.A. 101:1229-1234 (2004).
EMBL; AY489047; AAS15051.2; -..
GO; GO:0016220; G:membrane; IEA.
GO; GO:0016220; G:membrane; IEA.
InterPro; IPR00157; TIR.
SEQUENCE 707 AA; 79493 MW; 7D3BE21EE038F17E CRC64;
VINDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAALQPL
                                                                      LHTVKAGSPSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSSGLGEEE
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Mammalia, Butheria, Primates, Catarrhini, Hominidae,
NCBI_TaxID=9606;
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Pred. No. 2.8e-274;
1; Mismatches 1;
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101 ACHDQVAVTILWSPGALGIEFLKGFRVILEELKSEGROCQQLILKDPKQLNSSFKRTGME
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 Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godwaki P., "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins:
                                                                                                                                                                92.3%; Score 3703; DB 2; Length 728; 96.7%; Pred. No. 6.9e-274; ive 2; Mismatches 8; Indels 14
Wood
                                                        bioinformatics assessment.";
Genome Res. 13:2265-2270(12003).
BMBL; AY35874; AAG89134.1; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0004888; F:transmembrane receptor activity; IEA.
Interbro; IRR000157; TIR.
SEQUENCE 728 AA; 81310 MW; 4AD9D3F6B1C78C26 CRC64;
Yu G., Yuan J., Zhang M., Zhang Z., Goddard
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Best Local Similarity 96.7%;
Marches 702; Conservative
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                                 ALGIEFLKGFRVILEELKSEGROCOOLILKDPKOLNSSFKRTGMESOPFLNMKFETDYFV
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MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;

MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;

Chark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,

Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd Faton D., Poster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,

Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,

Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,

Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,

Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
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Momo sapiens (Human).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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QGUWIS;
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RESULT OF COMES OF CO

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507 482 567 542 627 602 687 662 747 722

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MESQPFINMKFETDYFVKVVPFPSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKPRN 218
                         LPRERLRPRPKVFLCYSSKDGONHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQRE 420
                                                    SSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEP-GQHT 539
                                                                                                                                                                                                                                            QPLILHAVKAGSPSEMPRDSGIYDSSVPSSELSLPLMEGLSPDQIETSSLTESVSSSGLG 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVLNDVISKPGPESDFCRKVEACVLGAAGPADSYSYLESQHVGLDQDTEAQPSCDSAPAL 643
                                                                                                                                                                                                                                                                                                                                         540 RQGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFEKQFVPFHPPPLRYREPVLEKFDSG
                                                                                                                                               QPLLHTVKAGSPSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSGLG
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2004 (TrEMBLrel. 27, Last amonotation update)
15-UTL-2004 (TrEMBLrel. 27, Last amonotation update)
17 receptor-like protein short form (Hypothetical protein bKRZp434L0320)
Name=IL17RLM; Synonyms=DKFZp434L0320;
Homo sapiens (Human).
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EMBL, AF494211; AAM74080.1; --
EMBL, AL83313; CAD38769.1; --
GOS GO: 0016020; C: Membrane; IEA.
GO; GO: 0004888; F: transmembrane receptor activity; IEA.
Interpro; IPR000157; TIR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu L., Chang Z.;
"hSef inhibits PC-12 cell differentiation by interfering with Ras-
mitogen-activated protein kinase MAPK signaling.";
J. Biol. Chem. 278:50273-50282(2003).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Pubmed=12598313; DOI=10.1074/jbc.M306936200;
Xiong S., Zhoo Q., Rong Z., Huang G., Huang Y., Chen P., Zhang Liu L., Chang Z.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
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SEQUENCE 595 AA; 66846 MW; 7E6BB64F73B2112 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EEDPPTLPSKLLASGVSR-EHGCHSHTDELQALAPL 738
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Matches 594; Conservative
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Q8N113;
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                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=21959295; Pubmed=11960706; DOI=10.1016/S0925-4773(02)00018-7;
Lin W., Furthauer M., Thisse B., Thisse C., Jing N., Ang S.-L.;
Lin W., Furthauer B. Sef gene and comparative analysis of its
expression with Fgf8 and Spry2 during embryogenesis.";
Mech. Dev. 113:163-168(2002).
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Xiong S., Zhao Q., Rong Z., Huang G., Huang Y., Chen P., Zhang S.,
Liu L., Chang Z.;
"NSef inhibits Pc-12 cell differentiation by interfering with Rasmitogen-activated protein kinase MAPK signaling.";
J. Biol. Chem. 278:50273-50282(2003).
                                                                                                                                                                      Craniata, Vertebrata, Euteleostomi;
Sciurognathi, Muridae; Murinae; Mus.
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
05-JUL-2004 (TrEMBL-El. 27, Last amoniation update)
Transmembrane protein (Interleukin 17 receptor-like protein long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84.8%; Score 3401.5; DB 2; Length 738; 85.4%; Pred. No. 7.6e-251; ive 37; Mismatches 52; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=BALB/c;
Xiong S.Q., Huang G.R., Zhao Q.H., Chen P.L., Rong Z.L., Ye X Chen Y., Liu L., Fu X.Y., Chang Z.J.;
Chen Y., Liu L., Fu X.Y., Chang Z.J.;
Submitted (MAR-2002) to the BMBL/GenBank/DDBJ databases.
EMBL; AF45944; AAM28441.1;
EMBL; AF45944; AAM28441.1;
EMBL; AF4594210; AAM74079.1;
CG; GO:0016021; C:integral to membrane; IEA.
GG; GO:00016021; C:integral to membrane; IEA.
GG; GO:0003676; F:uncleus; IEA.
GG; GO:000376; F:transmembrane receptor activity; IEA.
GG; GO:0008270; F:zinc ion binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             738 AA; 82347 MW; D8CE66230E3E8226 CRC64;
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                                                                                                                      Name=Ill7rd; Synonyms=Ill7rlm, Sef;
                                                                                                                                                                 Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
MCBI_TaxID=10090;
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InterPro; IPR007087; Znf C2H2.
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                                                                                                                                                  musculus (Mouse)
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181 PKVFLCYSSKDGQNHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQKIHES
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
FGF signaling antagonist SEF.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 370 PKVFLCYSSKDGQNHMAVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQKIHES
                                                                                                                                                                                                                                          QFIIVVCSKGMKYFVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKF
                                                                                                                                                                                                                                                                 241 QFIIVVCSKGMKYFVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKF
                                                                                                                                                                                                                                                                                                                       IAVYPDYSCEGDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFR
                                                                                                                                                                                                                                                                                                                                                                                                       SKSGRSLYVAICNMHQFIDEEPDWFEKQFVPFHPPPLRYREPVLEKFDSGLVLNDVMCKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         670 SDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSSGLGEEEPPALPSKLL
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                                                                               GPIRAVAITVPLVVISAFATLFTVMCRKKQQENIYSHLDEESSESSTYTAALPRERLRPR
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NCBI_TaxID=9031;
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Matches
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                                                                                   PGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKK 338
                                                                                                        QQENIYSHLDEESSESSTYTAALPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAYFLQDF 398
                                                                                                                                                                                                                                            CGCEVALDLWEDFSLCREGQREWVIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGGRGS 458
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                             LNISQHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTEMTSCLLQNVS
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                                                                                                                                                                                      QOENIYSHLDEESSESSTYTAALPRERLRPRPKVFLCYSSKDGONHWNVVQCFAYFLQDF
                                                                                                                                                                                                                                                                                                                            GKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMDNL
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Catarrhini, Hominidae, Homo.
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Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL133097; CAB61408.1;
PIR; T42695; T42695.
GO; GO:0016020; Cimembrane; IEA.
GO; GO:0004888; Fitransmembrane receptor activity; IEA.
Interpro; IPR000157; TIR.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp434N1928 (Fragment).
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Bukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates;
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                  SSYTKSNGLLNITFKYDNCTPYLNSVGKHVIGDVQNITISQYACYEQVAVTILWTANAIG 106
                                                                                     YALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQQENIYSHLDEESSESSTYT 358
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Sef protein (Fragment).
Name-SBF;
Gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                     IEFLKGFRVILEBLKSEGRQCQQLILKDPKQLNSSFKRTGMESQPFLNMKFETDYFVKVV
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GPASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVTILWSPGALG
                                                                                                                                          PFPSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKPRNLNISQHGSDMQVSFDHAPHN
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TISSUEFRACIAL mesenchyme;
MEDLINE-22651184; PubMed-12765832; DOI=10.1016/S0968-0004(03)00067-7;
Novatchkova M., Leibbrandt A., Werzowa J., Neubueser A.,
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Trends Biochem. Sci. 28:226-229(2003)
EMBL; AJ508679; CAD48485.1; -.
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                                                                                                                                                                                                                                                                                                                                        VVPFPSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKPRNLNISQHGSDMQVSFDHAP
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                                                                                                                                                        Gaps
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
                                                                                                                                                        4,
                                                                                                                    697;
                                                                                                                                                    Indels
                                                                                                                  Length
GO; GO:0016020; C:membrane; IEA.
GO; GO:0004888; F:transmembrane receptor activity; IEA.
InterPro; IFR00157; TIR.
NON TER
1 1
SEQÜENCE 697 AA; 79259 MW; D288939E1727F2C3 CRC64;
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0AR-2004 (TrEMBLrel. 26, Last annotation update)
Interleukin 17 receptor-like protein short form.
Name=Ill7rd, Synonyms=Ill7rm;
Mus musculus (Mouse).
                                                                                                                                                      92;
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                                                                                                                                                                                                                                                                       QQENIYSHLDEESSESSTYTAALPRERLRPRPKVFLCYSSKDGQNHWNVVQCFAYFLQDF 398
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                                                                                                                                                                                        LSTDOTETSSITESVSSSSGLGEEEPPALPSKLLSSGSCKADLGCRSYTDELHAVAPL 753
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                                                                                                                                                    DB 2; Length 594;
                                                                                                                                                   / Match 66.7%; Score 2675.5; DB 2; Length Local Similarity 84.8%; Pred. No. 1.6e-195; Ne 507; Conservative 34; Mismatches 50; Indels
                                                                                                                                     594 AA; 66780 MW; EABE6B655DCF4EC3 CRC64;
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                                                                      GO; GO: 0016020; C: membrane, GO; GO: 0016634; C: nucleus; GO; GO: 0003676; F: nucleic GO; GO: 0004888; F: transmemt GO; GO: 0008270; F: tinc ion InterPro; IPR00157; TIR. InterPro; IPR001697; ZIF.C.
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Q8R5J8;
01-JUN-2002 (
01-JUN-2002 (
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241 FSLCREGQREWAIQKIHESQFIIVVCSKGMKYFVDKKNFRHKGGSRGEAQGEFFLVAVAA
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                                                                                                                               Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                        | N. SEQUENCE FROM N.A. | SEQUENCE FROM N.A. |
| N. MEDLINE=21824237; PubMed=11802165; DOI=10.1038/ncb750; A Purthauer M., Lin W., Ang S.L., Thisse B., Thisse C.; |
| N. MEDLINE=21824237; PubMed=11802165; DOI=10.1038/ncb750; |
| N. Met. Cell Biol. 4:170-174(2002). |
| EMBL; AF424804; AAL79530.1; -. |
| ROD; MGD:016202; C:membrane; IEA. |
| ROD; MGD:0016202; C:membrane; IEA. |
| ROD; GO:0005634; C:nucleus; IEA. |
| ROD; GO:0005634; C:nucleus; IEA. |
| ROD; GO:0008207; F:zincleic acid binding; IEA. |
| ROD; GO:0008207; F:zincleic acid binding; IEA. |
| ROD; GO:0008207; TIR. |
| ROD; F:Zincleic S.T. |
| ROD; F:Zincle
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Similar expression to FGF protein (Fragment)
Name=1117rd; Synonyms=Sef;
Mus musculus (Mouse).
                                                                                                                          rus musculus (rouse).
Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFPSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKPRNLNISQHGSDMQVSFDHAPHN 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FGFRFFYLHYKLKHEGPFKRKTCKQEQTTETTSCLLQNVSPGDYIIELVDDTNTTRKVMH 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQQENIYSHLDEESSESSTYT 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AALPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQ 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VSAIAEKLROAKOSSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMDNLPQLCSHLHS 527
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                                                                                                                                                                                                                                                                                                                                                                   LAHFFMASCLFLCYTASVNG------GKRGNSDKCSYK-------QGTQT 43
                                                                                                                                                                                                                                                                                                                                                                                                           :|:|:||:||||:||||: |||| SAMDEGARKLGVIFRYDNCSVNWPIGKHAIHEVNNITFSHLSCDSQAAVVVHWMASPLG
                                                                                                                                                                                                                                                                                                                                           MAPWLQLCSVFFTVNACLNGSQLAVAAGGSGRARGADTCGWRMKAAARPRLCVANEGVGP
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                                                                                                                                                                                                                                                                                                                 Gaps
                                                                      Journal 117rd; Synonyms=sef;
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostel; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE-218218216; PubMed=11802164; DOI=10.1038/ncb749;

Teang M., Friesel R., Kudoh T., Dawid I.;

"Identification of Sef, a novel modulator of FGF signalling.";

Nat. Cell Biol. 4:165-169(2002).

EMBL, PAS44103; AAL76112.1; -.

ZFIN; ZBB-GENE-020320-5; ill7rd.

SEQUENCE 745 AA; 83431 MW; 56FEIF0B9D98DDB4 CRC64;
                                                                                                                                                                                                                                                                                                                 58;
                                                                                                                                                                                                                                                                                      Length 745;
                                                                                                                                                                                                                                                                                    Query Match
48.9%; Score 1961; DB 2; Length 7
Best Local Similarity 51.4%; Pred. No. 8.5e-141;
Matches 390; Conservative 114; Mismatches 197; Indels
                                      Last sequence update)
Last annotation update)
 745
                           Created)
                       (TrEMBLrel. 21, C
(TrEMBLrel. 21, I
(TrEMBLrel. 26, I
PRELIMINARY;
                                                                                                                                Cyprinidae; Dani
NCBI_TaxID=7955;
                        01-JUN-2002 (
01-JUN-2002 (
01-MAR-2004 (
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                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
48.6%; Score 1952; DB 2; Length 3
Best Local Similarity 51.1%; Pred. No. 4.2e-140;
Matches 388; Conservative 116; Mismatches 197; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fuerthauer M., Lin W., Siew-Lan A., Thisse B., Thisse C. Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF401232; AAL78817.1; -. ZFIN; ZDB-GENE-02030-5; ill7rd. SEQUENCE 745 AA, 83437 MW; 75BB9EDCC08A4652 CRC64;
                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                        TETSSLTESVSSSGLGEEEPPALPSKLLSSGS-CKADL
                                                                                                                                                                                                                                                              sequence update)
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                                                                                                                                                                                                                                  01-JUN 2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence up
01-MR-2004 (TrEMBLrel. 26, Last annotation
FOF signaling antagonist Sef.
Name=ill7rd; Synonyms=sef;
Brachydanio rerio (Zebrafish) (Danio rerio)
                                                                                                                                                                                   745
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                                                                                                                                                                                   PRELIMINARY;
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SEQUENCE FROM N.A.
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                                                                           ROLSLIDREPOPRVSKRNYFCSKSGRSLYVAIYNMHÖHVTÖEPDWLEKELM---PPPLP 579
                                                               588 YREPVLEKFDSGLVLINDVMCKPGPESDFCLKVEAAVL-----GATGPADSQHESQHGG 640
                                                                                                         641 LDQDGEARPALDGSAALQPLLHTVKAGSPSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQ 700
 SAIISEKLKEVHOKSS-DLSRFMSVYFDYSHETDVPTSLSLAPKFKLMDQLPQLFARLHS 522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASRNSGLYNITEKYDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVTILWSPGVL 103
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

TISSUB=Frontal lobe left;

MEDLINE=21458551; PubMed=11574149; DOI=10.1016/S0378-1119(01)00665-5;

MOSAGA N., Hida J., Tanuma R., Iseki K., Hirata M., Suto Y.,

Hirai M., Terao K., Suzuki Y., Sugano S., Hashimoto K.;

"Assignment of 118 novel cDNAs of cynomolgus monkey brain to human
                      528 RDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVALCNMHQFIDEEPDWFEKQFVPFHPPPLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAPWLQLCSVFFTVNACLNGSQLAVAAGGSGRARGADTCGWRMKAAARPRLCVANEGVGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Gaps
                                                                                                                                                                                                                                                         01-MAR-2003 (TrEWBLrel. 23, Last sequence update)
01-MAR-2003 (TrEWBLrel. 23, Last annotation update)
Hypothetical protein.
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE-Frontal lobe left;
Hashims-Frontal lobe left;
Bablims-to (N.C. Osada N., Hida M., Kusuda J., Sugano S.;
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AB093642; BAC21616.1; -.
Hypothetical protein.
SEQUENCE 109 AA; 11609 MW; 7EB13B49DB4C925B CRC64;
                                                                                                                                                               117R_HUMAN STANDARD; PRT; 866 AA.
096F46; 043844;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Interleukin-17 receptor precursor (IL-17 receptor).
Homo sapiens (Human).
                                                                                                                                                  701 TETSSLTESVSSSGLGEEEPPALPSKLLSSGS-CKADL 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 538; DB 2;
Pred. No. 2.9e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 13.4%; Score 538; DB Local Similarity 87.2%; Pred. No. 2.9e-les 102; Conservative 0; Mismatches
                                                                                                                                                                                                                                                   01-MAR-2003 (TrEMBLrel. 23, Created)
                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                             Cercopithecinae; Macaca
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene 275:31-37(2001).
                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                            chromosomes."
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RA MEDLINE=22388557; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA STRAUSBERG R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RIAMER R.D., Collins F.S., Wagner L., Sheamen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Romstein M.J., McEwan P.J., McKernan K.J., Maraman R.D., Mullahy S.J.,
R. Boask S.A., McEwan P.J., McKernan K.J., Maramson R.D., Mullahy S.J.,
R. Anthards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
R. Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
R. Althing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
R. McHander C. McTintulal L. Jones S.J.M., Marra M.A.;
R. McGeneration and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage, by, and for commercial,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; BC011624; AAH11624.1; -...
Genew; HGNC:5985; IL17R.
H-InvDB; HIX0016207; -...
MIM; 605461; -...
GO; GO:0005887; C:integral to plasma membrane; NAS.
GO; GO:0030368; P:interleukin-17 receptor activity; NAS.
GO; GO:000166; P:call surface receptor linked signal transdu.
Direct protein sequencing; Glycoprotein; Receptor; Signal;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=15340161; DOI=10.1110/ps.04682504; Zhang Z., Henzel W.J.; Zhang Z., Henzel W.J.; Rediction based on analysis of experimentally "Signal peptide prediction based on analysis of experimentally verified cleavage sites."; Protein Sci. 13:2819-2824(2004).
-: FUNCTION: Receptor for IL17. Binds its ligand with low affit
                                                                                                                                                                                                                                             MEDLINE=98035683; PubMed=9367539; DOI=10.1006/cyto.1997.0240; Yao Z., Spriggs M.K., Derry J.M.J., Strockbine L., Park L.S., Vanden Bos T., Zappone J., Painter S.L., Armitage R.J.; myolecular characterization of the human interleukin (II)-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Extracellular (Potential)
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Cytoplasmic (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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7.7%; Score 310; DB 1; Length 866;
Best Local Similarity 23.1%; Pred. No. 1.4e-14;
Matches 178; Conservative 107; Mismatches 338; Indels 146;
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Search completed: August 9, 2005, 11:48:50 Job time: 123.76 secs

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SUMMARIES	Descr	ABB07626 Human	ABB07627 Human	ABB07628 Human	AAU09904 Human	19953 Auman Aau09953 Human	AAU09954 Human	AAU09951 Human	AAU09952 Human	AAU09956 Auman	AAU09957 Human	Aau0995		AAU04958 Human		ABU72600 Human	3241 Ada43241 Human	ADA49782 Human	ADA26975 Human	ADB66909 ADB66909 Human	ABW02061 Human	3 Adg8739	ADL16689 Human	ADL16650 Human	ADL71310 Adl71310 Human	
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ALIGNMENTS

The invention relates to an isolated cytokine receptor polypeptide designated Zcytori8. The Zcytori8 polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with porisists or tumour growth. The encoding nucleic acids are useful for providing Zcytori8 in vivo by gene therapy techniques. Zcytori8 oligonucleotide probes are useful for in vivo diagnosis, and the Zcytori8 probes and primers can be used to detect and localize Zcytori8 gene expression in tissue samples. The probes are also useful for detecting gross aberrations in chromosome 3 in which zcytori8 gene resides. The Zcytori8 polynucleotides can also be used in linkage-based testing of pulmonary alveolar proteinosis, familial growth, Cytokine receptor; Zcytor18; cell proliferation; antipsoriatic; human; pulmonary alveolar proteinosis; familial periodic fever; antitumour; erythroleukemia; chromosome 3p14.3; gene therapy. New cytokine receptor polypeptide designated zcytor18, useful for inhibiting cell proliferation associated with psoriasis or tumor growt and modulating immune system by binding to endogenous zcytor18 ligand. Human cytokine receptor, Zcytor18 amino acid sequence. ABB07626 standard; protein; 753 AA 2; Gao Claim 1; Page 2; 119pp; English. 26-JUL-2000; 2000US-0220747P. 23-JUL-2001; 2001WO-US023253. N-PSDB; ABA95031, ABA95032. Presnell SR, Kuestner RE, (first entry) (ZYMO) ZYMOGENETICS INC. WPI; 2002-217048/27. WO200208259-A2. Homo sapiens. 31-JAN-2002. 20-MAY-2002 ABB07626; ABB07626

Homo sapiens

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  erythroleukemia associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytokine receptor; Zcytor18; cell proliferation; antipsoriatic; human; pulmonary alveolar proteinosis; familial periodic fever; antitumour; erythroleukemia; chromosome 3p14.3; gene therapy; variant.
                                                                                                                                                                                                                                             PRNLNI SQHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTETTSCLLQ
                                                                                                             1 ADTCGWRMKAAARPRLCVANEGVGPASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNI
                                                                                                                         36 ADTCGWRWKAAARPRLCVANEGVGPASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNI
periodic fever and erythroleukemia, and erythroleukemia associated wi
polymorphisms of cytokine receptors. The present sequence represents
human Zcytor18 amino acid sequence
                                                                                         Gaps
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                                                                   Length 753;
                                                                                       Indels
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The invention relates to an isolated cytokine receptor polypeptide designated Zcytor18. The Zcytor18 polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with psoriasis or tumour growth. The encoding nucleic acids are useful for providing Zcytor18 in vivo by gene therapy techniques. Zcytor18 oligonucleotide probes are useful for invivo diagnosis, and the Zcytor18 probes and primers can be used to detect and localize Zcytor18 gene expression in tissue samples. The probes are also useful for detecting gross aberrations in chromosome 3 in which Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in linkage-based testing of pulmonary alveolar proteinosis, familial periodic fever and erythroleukemia, and erythroleukemia associated with polymorphisms of cytokine receptors. The present sequence represents a human Zcytor18 variant amino acid sequence
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ive 0; Mismatches
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Location/Qualifiers
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The invention relates to an isolated cytokine receptor polypeptide designated Zcytor18. The Zcytor18 polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with psoriation tumour growth. The encoding nucleic acids are useful for providing Zcytor18 in vivo by gene therapy techniques. Zcytor18 oligonucleotide probes are useful for in vivo diagnosis, and the Zcytor18 probes and primers can be used to detect and localize Zcytor18 gene expression in tissue samples. The probes are
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                                                                                                                                                                                                                                                                                                                   Cytokine receptor; Zcytor18; cell proliferation; antipsoriatic; human; pulmonary alveolar proteinosis; familial periodic fever; antitumour; erythroleukemia; chromosome 3p14.3; gene therapy; splice variant.
DNLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFE
                                                                                                                                                            QDFCGCEVALDLWEDFSLCREGQREWVIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGG
                                                                                                         Human cytokine receptor, Zcytor18 splice variant
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also useful for detecting gross aberrations in chromosome 3 in which Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used linkage-based testing of pulmonary alveolar proteinosis, familial periodic fever and erythroleukemia, and erythroleukemia associated wipolymorphisms of cytokine receptors. The present sequence represents human Zcytor18 splice variant
                                                                                                                                                          1 ADTCGWRMKAAARPKLCVANEGVGPASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNI
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                                                                                                           Length 739;
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                                                                                                             Query Match
                                                                                                                                     Matches
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The invention describes novel nucleic acids encoding interleukin (IL) 17
receptor like polypeptides useful as vaccines and in gene therapy. These
receptor like polypeptides useful as vaccines and in gene therapy. These
contembration anti-convulsant, anti-alzabetic, anti-alzabeimer's, renal,
immunosuppressive, hepatic, anabolic, anorectic, anti-alzabeimer's, renal,
costeopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and
coptumental section anti-convulsant, anti-leukaemic, anti-infertility and
coptutal mological activities. The IL-17 receptor like nucleic acids and
coptutal mological activities. The IL-17 receptor like polypeptide (IL177th) expression. These
conclude, for example immune disorders (e.g. inflammation diabetes and
cransplant rejection), infections (e.g. hepatitis and septicaemia),
weight disorders (e.g. anorexia, cachexia and obesity),
conclude disorders (e.g. anorexia, sathma and emphysemal, skin disease
concers, cachesis, sathma and emphysemal, skin disease
concers, cachesis, and hypercalcaemia, wascular disorders
(e.g. erroke and atherosclerosis, and hypercalcaemia), vascular disorders
(e.g. erroke and atherosclerosis, and retinal neuropathy). The
complements may also used as diagnostic probes to detect and
concers needing restorative therapy. The IL17Th may also be used as
cantigens in the production of antibodies against the proteins and in
cassays to identify modulators of expression and activity. The anti-
concers and antagonists may also be used to down assays to identify modulators of a suppression and activity. The anti-
concers and antagonists may also be used as one set of down and an antagonists may also be used as diagnostic probes to detect and
concers and enterprocative therapy. The IL17Th may also be used as
cantigens in the production of antibodies against the proteins and in
assays to identify modulators of expression and activity. The anti-
concers and antagonists may also be used as enterpression and enterpression and articity and antagonists may also be used as
               hepatic; anabolic; ancrectic; anti-alzheimer's; anti-parkinsonian; anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic; ascular; cytostatic; anti-leukamenc; anti-infertility; ophthalmological; hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease; bone disease; vascular disorder; eye disorder; cancer; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psoriasis and glaucoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ILI7rlp antibodies and antagonists may also be used to down regulate expression and activity. This is the amino acid sequence of the human Interleukin 17 (IL-17) receptor like protein described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 DICGWRMKAAARPRLCVANEGVGPASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 3725;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Page 152-154; 158pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.3%;
97.8%;
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2000US-00724460
                                                                                                                                                                                                                                                                                                                   15-MAR-2001; 2001WO-US008678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-611392/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                              (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-611392/
N-PSDB; AAS15346.
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                                                                                                                                                                      Homo sapiens.
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28-NOV-2000;
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Best Local 9
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ISQYACHDQVAVTILMSPGALGIEFLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFKR 142 62 ISQYACHDQVAVTILWSPGALGIEFLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFKR 121

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Interleukin 17; hIL-17 receptor like protein; immunomodulatory; anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial; hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian; anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic; vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological; hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease; bone disease; vascular disorder; eye disorder; cancer; human; mutant;
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                                                                                                                                                                                  KKQQENIYSHLDEESSESSTYTAALPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAYFLQ 361
                                                                                                                                                                                                                                                                                                       481
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                                                                                                                                                                                                                                                                                                                                                                                              NLPQLCSHIHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFEK 562
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TGMESQPFLINMKFETDYFVKVVPFPSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKP
                  TGMESQPFLNMKFETDYFVKVVPFPSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKP
                                                                                  RNINISQHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTETTSCLLQN
                                                                                                                                        VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAMAITVPLVVISAPATLFTVMCR
                                                                                                                                                                                                                                                                         DFCGCEVALDLWEDFSLCREGQREWVIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                 OFVPFHPPPLRYREPVLEKFDSGLVLNDVMCKPGPESDFCLKVFAPVLGATGPADSQHES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNLNISQHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTETTSCLLQN
                                                                                                                      VSPGDYI I ELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVI SAFATLFTVMCR
                                                                                                                                                                                                                                              DFCGCEVALDLWEDFSLCREGOREWVIOKIHESQFIIVVCSKGMKYFVDKKNYKHKGGGR
                                                                                                                                                                                                                                                                                                           GSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMD
                                                                                                                                                                                                                                                                                                                                                                                                                              QFVPFHPPPLRYREPVLEKFDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QHGGLDQDGEARPALDGSAALQPLLHTVKAGSPSDMPRDSGIYDSSVPSSELSLPLMEGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STDQTETSSLTESVSSSSGLGEEEPPALPSKLLSSGSCKADLGCRSYTDELHAVAP 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STDQTETSSLTESVSSSGLGEEEPPALPSKLLSSGSCKADLGCRSYTDELHAVAP 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Interleukin 17 (hIL-17) receptor like protein substitution #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Ser, Thr, Ala, Cys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU09953 standard; protein; 738 AA.
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The invention describes novel nucleic acids encoding interleukin (IL) 17
receptor like polypeptides useful as vaccines and in gene therapy. These
receptor like polypeptides useful as vaccines and in gene therapy. These
convenient inflammatory, anti-diabetic, anti-microbial,
immunosuppressive, hepatic, anabolic, ancrectic, anti-alzheimer's, renal,
anti-parkinsonian, anti-convulsant, anti-alsthematic), dermatcological,
costeopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and
optical activities. The IL-17 receptor like nucleic acids and
coptens may be used to prevent and treat diseases associated with
inappropriate IL-17 receptor like polypeptide (IL17Tp) expression. These
coptens may be used to prevent and disorders (e.g. inflammation, diabetes and
transplant rejection), infections (e.g. papatitis and septicaemia),
weight disorders (e.g. anorexia, cachexia and obesity), neuronal
cransplant rejection), infections (e.g. parkinson's disease and epilepsy),
lung disorders (e.g. cystic fibrosis, serkima and emphysema), skin disease
coptenders (e.g. oxteoporosis, asthema and emphysema),
clung disorders (e.g. oxteoporosis and hypercalcaemia), vascular disorders
(e.g. stroke and atherosclerosis, cancers (e.g. infertility and
chreast cancer), reproductive disorders (e.g. infertility and
chreast cancer), reproductive disorders (e.g. infertility and
chreat cancer), reproductive disorders (e.g. infertility and
chreat cancer), reproductive disorders (e.g. infertility and
cynamitate the presence of similar nucleic acids in samples and identify
patients needing restorative therapy. The IL17Ip may also be used as
considered to dentify modulators of expression and activity. The anti-
coptication but is based on the human interleuking to copy or expression and activity. Note: This sequence is not given in the
capeatic processing the producer (AMU09904) and has been created according to
copy information given in claim 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82
                                                                                                                                                                                                        acids encoding interleukin 17 receptor like polypeptides, useful renting, diagnosing and treating, e.g. leukemia, asthma, diabetes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAMAITVPLVVISAFATLFTVMCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISQYACHDQVAVTILWSPGALGIEFLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFKR
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Pred. No. 0;
1; Mismatches 2; Indels 1
                                                                                                                                                                                                                                                                                                 Page; 158pp; English.
                    16-MAR-2000; 2000US-0189816P.
28-NOV-2000; 2000US-00724460.
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Matches 699; Conservative
                                                                                                                                                                                                                                                         psoriasis and glaucoma.
                                                                                                                                                                    WPI; 2001-611392/70.
                                                                                (AMGE-) AMGEN INC
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anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial; hepatic; anabolic; ancectic; anti-alzheimer's; anti-parkinsonian; anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic; vascular; cytostatic; anti-leukamic; anti-infertility; ophthalmological; hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease; bone disease; vascular disorder; eye disorder; cancer; human; mutant;
                                                                                                                                    442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       622
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NLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFEK
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                                                                                                                                                                                             GSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMD
                                                                                                                                                                                                                            QFVPFHPPPLRYREPVLEKFDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHES
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                                                                                    DFCGCEVALDLWEDFSLCREGQREWVIQKIHESQF1IVVCSKGMKYFVDKKNYKHKGGGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human Interleukin 17 (hIL-17) receptor like protein substitution #4.
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28-NOV-2000; 2000US-00724460.
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The invention describes novel nucleic acids encoding interleukin (IL) 17
receptor like polypeptides useful as vaccines and in gene therapy. These
receptor like polypeptides useful as vaccines and in gene therapy. These
contemporate inflammatory, anti-inflammatory, anti-inflammatory, anti-inflammatory, anti-inflammatory, anti-inflammatory, anti-inflammatory, anti-inflammatory, anti-inflammatory, anti-inflammatory, dermatological,
anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
costeopathic, vascular, cytostatic, anti-luekaemic, anti-infertility and
cophthalmological activities. The IL-17 receptor like nucleic acids and
cophthalmological activities. The IL-17 receptor like nucleic acids and
cophthalmological activities. The LI-17 receptor like nucleic acids and
cophthalmological activities. The LI-17 receptor like nucleic acids and
cophthalmological activities. The LI-17 receptor like nucleic acids and
cophthalmological activities and elso described include, for example immune disorders (e.g. hepatitis and septicaemia),
weight disorders (e.g. anorexia, cachexia and obesity), neuronal
dysfunction (e.g. albeimer's disease, parkinson's disease and epilepsy),
cophen disorders (e.g. osteoporosis, asthma and emphysema), skin disease
(e.g. erzema and psoriasis), kidney disease (e.g. glomerulonephritis),
cophen diseases (e.g. osteoporosis and hypercalecemia, myeloma and
copheranticate the presence of similar nucleic acids in samples and identify
copatients needing restorative therapy. The ILI7Th may also be used as
contitates needing restorative therapy. The ILI7Th may also be used as
cancers of similar nucleic acids in samples and in
assays to identify modulators of expression and activity. The anti-
cophthalmologies and antagonists may also be used to down regulate
expression and activity. Note: This sequence is not given in the
capture species on the human Interleukin 17 (IL-17) receptor
cophthalmologies.
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97.6%; Pred. No. 0;
Claim 21; Page; 158pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    information given in claim 21
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Matches 699; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 738 AA;
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Best Local (
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The invention describes novel nucleic acids encoding interleukin (IL) 17 receptor like polypeptides useful as vaccines and in gene therapy. These have immunomodulacory, anti-inflammatory, anti-diabetic, anti-microbial, immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal, anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological, osteopathic, vascular, cytostatic, anti-laukaemic, anti-infertility and ophthalmological activities. The IL-17 receptor like nucleic acids and proteins may be used to prevent and treat diseases associated with inappropriate IL-17 receptor like polypeptide (IL17tlp) expression. These include, for example immune disorders (e.g. inflammation, diabetes and transplant rejection), infections (e.g. hepaticis and septicaemia), weight disorders (e.g. anorexia, cachexia and obesity), neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                             Interleukin 17; hIL-17 receptor like protein; immunomodulatory; anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial; hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian; anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic; vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological; hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease; bone disease; vascular disorder; eye disorder; cancer; human; mutant;
                                   622
                                                                        199
                                                                                                             682
601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes,
                                                                                                             OHGGLDODGEARPALDGSAALQPLLHTVKAGSPSDMPRDSGIYDSSVPSSELSLPLMEGL
QFVPFHPPPLRYREPVLEKFDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHES
                     563 OFVPFHPPPLRYREPVLEKFDSGLVLNDVMCKPGPESDFCLKVEAPVLGATGPADSQHES
                                                                        OHGGLDODGEARPALDGSAALQPLLHTVKAGSPSDMPRDSGIYDSSVPSSELSLPLMEGL
                                                                                                                                                  STDQTETSSLTESVSSSSGLGEEPPALPSKLLSSGSCKADLGCRSYTDELHAVAP 717
                                                                                                                                                                     Human Interleukin 17 (hIL-17) receptor like protein substitution #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Gly, Pro or Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                     AAU09951 standard; protein; 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 18; Page; 158pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-MAR-2000; 2000US-0189816P.
28-NOV-2000; 2000US-00724460.
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                                                                                                                                                                                                                                                                                                                                                             14-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            psoriasis and glaucoma
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482 NLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFEK

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dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),

lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease

(e.g. eczema and psociasis), kidney disease (e.g. glomerulonephritis),

bone diseases (e.g. osteoporosis and hypercalcaemia), wascular disorders

(e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and

breast cancer), reproductive disorders (e.g. infertility and

miscarriage), eye disporders (e.g. glaucoma and retinal neuropathy). The

DNA and its complements may also used as diagnostic probes to detect and

cup antitate the presence of similar nucleic acids in samples and identify

patients needing restorative therapy. The ILI77Lp may also be used as

antigens in the production of antibodies against the proteins and in

cassays to identify modulators of expression and activity. The anti-

CILI71Lp antibodies and antagonists may also be used to down regulate

expression and activity. Note: This sequence is not given in the

specification but is based on the human Interleukin 17 (IL-17) receptor

cinformation given in claim 18
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Sequence 738 AA;

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                                                                                                                                              ISQYACHDQVAVTILWSPGALGIEFLKGFRVILEELKSEGRQCQQLILKDFKQLNSSFKR 142
                                                                                                                                                                                                                                RNLNISOHGSDMOVSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTETTSCLLQN 241
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                                                                                                                                                                                                                                                                                                                                                                                                 DFCGCEVALDLWEDFSLCREGQREWVIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGGR 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMD 481
                                                                                                                                                                            TGMESQPFLNMKFETDYFVKVVPFPSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKP 181
                                                                                                                                                                                                    TGMESQPFLNMKFETDYFVKVVPFPSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKP 202
                                                                                                                                                                                                                                                                                     VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCR 301
                                                                                        DICGWR------GVXPASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNIT 82
                                                                                                                                                                                                                                                                                                                                                                                                                    NLPQLCSHLHSRDHGLQBPGQHTRQGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFBK
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                                                                 DICGWRMKAAARPRLCVANEGVGPASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNIT
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                                       Gaps
                                      2; Indels 14;
            DB 4; Length 738;
Score 3718; D
                         Pred. No. 0;
1; Mismatches
            Query Match
Best Local Similarity 97.6%;
Matches 699; Conservative
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processing may be used to prevent and trace there are accessed associated for inappropriate IL-17 receptor like polypeptide (ILI7IP) expression. These include, for example immune disorders (e.g. inflammation, diabetes and transplant rejection), infections (e.g. inflammation, diabetes and controlled to transplant rejection), infections (e.g. inflammation, diabetes and experienced dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy), dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy), confidenced (e.g. asthma and emplysema), wind disease (e.g. gretce fibrosis, asthma and emplysema), with disease (e.g. extroke and apportants), kidney disease (e.g. elevental), vascular disorders (e.g. etroke and atherosoclerosis, cancers (e.g. leukemia, myeloma and breast cancer), reproductive disorders (e.g. infertility and construction may also used as diagnostic probes to detect and quantitate the presence of similar nucleic acids in samples and identify cancers in the production of antibodies againet the proteins and in antigens in the production of antibodies againet the proteins and incompanies and antiagonists may also be used to down regulate (ILI7TIP) antibodies and antagonists may also be used to down regulate expression and activity. Note: This sequence is not given in the
                                                                                                                                                                                                                Interleukin 17; hIL-17 receptor like protein; immunomodulatory; anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial; hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian; anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic; vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological; hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease; bone disease; vascular disorder; eye disorder; cancer; human; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention describes novel nucleic acids encoding interleukin (IL) 17 receptor like polypeptides useful as vaccines and in gene therapy. These inmunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial, immunosuppressive, hepatic, anti-inflammatory, anti-alzhaimer's, renal, anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological, anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological, ophthalmological activities The IL-17 receptor like nucleic acids and proteins may be used to prevent and treat diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes.
                                                                                                                                                                         Human Interleukin 17 (hIL-17) receptor like protein substitution #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Phe, Leu, Val, Ile, Ala, Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
Misc-difference 227
                                            AAU09952 standard; protein; 738 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 19; Page; 158pp; English.
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28-NOV-2000; 2000US-00724460.
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                                                                                                                                     (first entry)
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psoriasis and glaucoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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RESULT 8
AAU09952
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ascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological;

hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease; bone disease; vascular disorder; eye disorder; cancer; human; mutant;

Location/Qualifiers /label= Asp, Glu

Misc-difference 51

sapiens

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mutein.

Synthetic.

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16-MAR-2000; 2000US-0189816P. 28-NOV-2000; 2000US-00724460. 15-MAR-2001; 2001WO-US008678

(AMGE-) AMGEN INC.

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                                                                                                                                                                      93 ISQYACHDQVAVTILWSPGALGIEFLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFKR 142
                                                                                                                                                                                                       TGMESOPFILMMKFETDYFVKVVVPPPSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKP 202
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                                                                                                                                                                                                                                                   RNLNISQHGSDMQVSFDHAPHNFGXRFFYLHYKLKHEGPFKRKTCKQEQTTETTSCLLQN 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     NLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFEK 541
                                                                                                                                                                                                                                                                               VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCR 301
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                                                                                                                                                                                                                                                                                                                                                                 DFCGCEVALDLWEDFSLCREGQREWVIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGGR 421
                                                                                                                                                                                                                                                                                                                                                                                                            GSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMD 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIPQLCSHIHSKDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFEK 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QEVPPHPPPLRYREPVLEKFDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHES 601
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                                                                                                                           DICGWR------GVGPASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNIT 82
Interleukin 17 (IL-17) receptor
                                                                                                                                                                                          TGMESQPFLNMKFETDYFVKVVPFPSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKP
                                                                                                        DICGWRMKAAARPRLCVANEGVGPASRNSGLYNITPKYDNCTTYLNPVGKHVIADAQNIT
                                                                                                                                                 62 ISQYACHDQVAVTILWSPGALGIEFLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFKR
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                                                                                   Gaps
      like protein sequence (AAV09904) and has been created according to information given in claim 19
                                                                                   14;
                                                               Length 738;
                                                                                   2; Indels
                                                               4.
                                                               B
                                                             Score 3718; DB
Pred. No. 0;
1; Mismatches
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specification but
                                          Sequence 738 AA;
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Matches 699
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The invention describes mover macracia across and in gene therapy. These have immunosuppressive, hepatic, anti-inflammatory, anti-diabetic, anti-microbial, immunosuppressive, hepatic, anti-inflammatory, anti-diabetic, anti-microbial, immunosuppressive, hepatic, andi-asthmatic, dermatological, cstrivties. The IL-IT receptor like mucleic acids and proteins may be used to prevent and treat diseases associated with imappropriate IL-IT receptor like mucleic acids and proteins may be used to prevent and treat diseases associated with inflammation, diabetes and transplant rejection) infections (e.g. hepatitis and septicaemia), weight disorders (e.g. anorexia, cachexia and obesity), neuronal (e.g. Alzheimer's disease, Parkinson's disease and epilepsy), lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis), bone diseases (e.g. cystic fibrosis, asthma and emphysema), skin disease (e.g. excemportosis, asthma and emphysema), skin disease (e.g. stroke and atheroscierosis, asthma and emphysema), skin disease (e.g. stroke and atheroscierosis, cancers (e.g. infertility and breath and its complements may also used as diagnostic probes to detect and breath its complements may also used as infertility and its complements may also used as diagnostic probes to identify modulators of similar nucleic acids in samples and in assays to identify modulators of expression and activity. The anti-complement in the production of antibodies against the proteins and in assays to identify modulators of expression and activity. The anti-complement is based on the human incerlenkin if (IL-IT) receptor in the protein sequence (Allan and according to complements may also be used to down regulate expression and activity. Note: This sequence is not given in the protein sequence (Allan and according to complements may also be used to down regulate expression and activity. Note: This sequence is not given in the protein sequence (Allan and according to complements
Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psoriasis and glaucoma.
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                                                                                                                                                                                                                                                                                 The invention describes novel nucleic acids encoding interleukin (IL) 17
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                                                                                                                                                                                         Claim 23; Page; 158pp; English.
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Matches 699; Conservative
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anti-inflammatory, anti-diabetic; immunosuppressive; anti-microbial; hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian; anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;

Interleukin 17; hIL-17 receptor like protein; immunomodulatory;

Human Interleukin 17 (hIL-17) receptor like protein substitution #6.

(first entry)

14-FEB-2002

AAU09956;

AAU09956 standard; protein; 738 AA

15-MAR-2001; 2001WO-US008678 16-MAR-2000; 2000US-0189816P. 28-NOV-2000; 2000US-00724460.

20-SEP-2001

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KKQQENIYSHLDEESSESSTYTAALPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAYFLQ 382
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ISQYACHDQVAVTILMSPGALGIEFLKGFRVILEELKSEGRQCQQLILKOPKQLNSSFKR 142
                            181
                                                                                                                                       RNLNISQHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTETTSCLLQN 241
                                                                                                                         VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCR 301
                                                                                                                                                                         KKQQENIYSHLDEESSESSTYTAALPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAYFLQ 361
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                            TGMESQPFLNMKFETDYFVKVVPFPSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKP
                                        TGMESQPFLNMKFETDYFVKVVPFPSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKP
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The invention describes novel nucleic acids encoding interleukin (IL) 17
receptor like polypeptides useful as vaccines and in gene therapy. These
have immunoadulatory, anti-inflammatory, anti-diabetic, anti-microbial,
immunosuppressive, hepatic, anabolic, anci-diabetic, anti-infertility and
conti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and
ophthalmological activities. The IL-17 receptor like nucleic acids and
copteins may be used to prevent and treat diseases associated with
inappropriate IL-17 receptor like polypeptide (IL17rb) expression. These
copteins may be used to prevent and treat diseases associated with
infections (e.g. inflammation, diabetes and
transplant rejection), infections (e.g. hepatitis and septicaemia),
weight disorders (e.g. anorexia, cachexia and obesity), neuronal
dysfunction (e.g. Alzheimer's disease, parkinson's disease and epilepsy),
copied diseases (e.g. osteoporosis, aethma and emphysema), skin disease
(e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
copied diseases (e.g. osteoporosis and hypercalcaemia), wascular disorders
(e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and
breast cancer), reproductive disorders (e.g. leukemia, myeloma and
copied as atroke and atherosclerosis, cancers (e.g. leukemia, myeloma
copied and the presence of similar nucleic acids in samples and identify
copied antigens in the production of antibodies against the proteins and in
copied antigens in the production of antibodies against the proteins and in
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copied antigens in the arminors of expression and activity. The anticopied antigens in the production of antibodies against the proteins and in the
copied antigens in the arminors of expression and activity. The propession and artegorial production of antibodies against the arminors of expression and a

Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes,

Claim 24; Page; 158pp; English.

for preventing, diagnos. psoriasis and glaucoma.

WPI; 2001-611392/70

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(AMGE-) AMGEN INC

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Interleukin 17; hIL-17 receptor like protein; immunomodulatory; anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial; hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian; anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic; vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological; hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease; bone disease; vascular disorder; eye disorder; cancer; human; mutant;
                                                                                                                   Human Interleukin 17 (hIL-17) receptor like protein substitution #7.
                            AAU09957 gtandard; protein; 738 AA
                                                                                          (first entry)
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RESULT 10
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/label= Cys, Ala, Ser Location/Qualifiers

Misc-difference

Synthetic

WO200168859-A2

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VSPGDXIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCR 301
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                                                                                                                                                                                                                                                                                                                                                                                                                expression and activity. Note: This sequence is not given in the specification but is based on the human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904) and has been created according to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DICGWR-------GVGPASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNIT
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97.6%; Pred. No. 0;
ive 1; Mismatches
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preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes,

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Interleukin 17; hIL-17 receptor like protein; immunomodulatory; anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial; hepatic; anabolic; ancettic; anti-alzheimer's; anti-parkinsonian; anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic; vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological; hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease; bone disease; vascular disorder; eye disorder; cancer; human; mutant;
                                         DFCGCEVALDL#EDFSLCREGQREWVIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGGR 442
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VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAMAITVPLVVISAFATLFTVMCR 322
                        KKQQENIYSHLDEESSESTYTAALPRERLRPRPKVFLCYSSKDGQNHMVVVQCFAYFLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Interleukin 17 (hIL-17) receptor like protein substitution #5
                                                                                                                               GSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGI
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2000US-00724460.
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Nucleic acids encoding interleukin 17 receptor like polypeptides, useful

WPI; 2001-611392/70.

(AMGE-) AMGEN INC

Jing S;

28-NOV-2000;

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The invention describes novel nucleic acids encoding interleukin (IL) 17

receptor like polypeptides useful as vaccines and in gene therapy. These
have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
immunosuppressive, hepatic, anti-alsthmatic, dermatological,
osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and
ophthalmological activities. The IL-17 receptor like nucleic acids and
proteins may be used to prevent and treat diseases associated with
inappropriate IL-17 receptor like polypeptide (ILI7rlp) expression. These
include, for example immune disorders (e.g. inflammation, diabetes and
transplant rejection), infections (e.g. hepatitis and septicaemia),
weight disorders (e.g. anorexia, cacheraia and obesity), neuronal
dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
(e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
con receptor in reproductive disorders (e.g. infertility and
con disease cancer), reproductive disorders (e.g. infertility and
con disease (e.g. osteoporosis and hypercalcaemia), myeloma and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  miscarriage), eye disorders (e.g. glaucome and retinal neuropathy). The DNA and its complements may also used as diagnostic probes to detect and quantitate the presence of similar nucleic acids in samples and identify patients needing restorative therapy. The LL17rlp may also be used as antigens in the production of antibodies against the proteins and in assays to identify modulators of expression and activity. The anti-ll17rlp antibodies and antagonists may also be used to down regulate expression and activity. Note: This sequence is not given in the specification but is based on the human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904) and has been created according to
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97.6%; Pred. No. 0;
cive 1; Mismatches
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                                                                      Page; 158pp;
                      psoriasis and glaucoma
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                                                                                                                                                                                                                                                                                                                                  Human, pharmaceutical, diagnostic, gene therapy, tissue regeneration, cell regeneration, membrane protein, signal transduction-related protein, transcription related protein, osteoporosis, neurological disease,
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              NLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFEK
                                                 QFVPFHPPPLRYREPVLEKFDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHES
                                                               QFVPFHPPPLRYREPVLEKFDSGLVLNDVMCKPGPESDFCLKVEAPVLGATGPADSQHES
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Hio Y, Otsuka K, Nagai K, Irie R,
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                              protein encoded by clone TESTI20046540.
                                                                                                                                                                                                                                       ADB65245 standard; protein; 728 AA
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(REAS-) RES ASSOC BIOTECHNOLOGY.
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25-JAN-2002; 2002US-00350978.
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                                                                                                                                                                                                                                                                                                                                                                               cancer; tumour
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Yamamoto J,
Seki N, Yosh
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regeneration. Membrane proteins, signal transduction-related proteins, transcription-related proteins, disease-related proteins and genes encoding them can be used as indicators for diseases (e.g. osteoporosis, neurological diseases, cancer, tumours. The cDNA may be used to regulate the activity or expression of the encoded protein to treat diseases. The sequence presented is a protein of the invention. Note: Some of the sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 ALGIEFLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFKRTGMESQPFLNMKFETDYFV 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGQREWVIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKL
                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                            Length 728;
                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGEEEPPALPSKLLSSGSCKADLGCRSYTDELHAVAPL
                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                      Score 3708; E
                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU04958 standard; protein; 728
                                                                                                                                                                                                                                                                                          96.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 99.7
Matches 696; Conservative
                                                                                                                                                                                                                                              Sequence 728 AA;
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Grimaldi CJ; Vandlen RL;

Human

Region

Region

Domain Region
```
The sequence is PRO20026 which is the human Interleukin 17 receptor, IL-
17RH4, encoded by DNA 154095-2998. A composition containing ant/agonists
to the PRO polypeptides or individual components are useful for treating
a mammal with an immune related disease, e.g. systemic lupus
erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic
arthritis, a spondyloarthropathy, systemic sclerosis, an idiopathic
inflammatory myopathy, Sjogram's syndrome, systemic vasculitis,
sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia,
thyroiditis, diabetes mellitus, immune-mediated skin disease,
contact dermatitis, an allergic disease e.g. food hypersensitivity,
asthma, a transplantation associated disease, or a chronic inflammatory
demyelinating polymeuropathy. Treating a degenerative cartilaginous
disorder comprises administering a PRO1031 or PRO1122 polypeptide
agonist, or antagonist to the mammal. Numerous examples of the diseases
and disorders are given in the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NYKHKGGGRGSCKGELFLVAVSAIAEKURQAKQSSSAALSKFIAVYFDYSCEGDVPGILD 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQKIHESQFIIVVCSKGMKYFVDKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RASASGVPALFVSGEQGVGPASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNITISQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACHDOVAVTILWSPGALGIEFLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFKRTGME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 SQPFLNMKFETDYFVKVVPFPSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKPRNLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 EMTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATLFTVMCRKKQQENIYSHLDEESSESSTYTAALPRERLRPRPKVFLCYSSKDGQNHMNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQKIHESQFIIVVCSKGMKYFVDKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 RMKAAARPRLCVANE-GVGPASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNITISQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 ISQ------HGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF
                                                                                                                                                                                                                                      Novel PRO polypeptides homologous to interleukin-17, useful for the diagnosis and treatment of immune related disease e.g. rheumatoid arthritis and diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 728;
                                                                                                                    Filvaroff E, Fong S, Goddard A, Godowski FJ,
,, Li H, Hillan KJ, Tumas D, Van Lookeren M,
CK, Williams PM, Wood WI, Yansura DG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 3703;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                      Claim 10; Fig 18; 188pp; English.
            10-NOV-2000; 2000W0-US030873.
28-NOV-2000; 2000US-0253646P.
01-DEC-2000; 2000WO-US032678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96.7%;
ilarity 96.7%;
Conservative 2
                                                                                      (GETH ) GENENTECH INC.
                                                                                                                                                                                                WPI; 2001-451708/48.
N-PSDB; AAS09517.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 702; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 728 AA;
                                                                                                                                          Gurney AL, L
Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123
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                                                                                                                           'n,
                                                                                                                           Chen
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "cAMP/GMP-dependent protein kinase phosphorylation
                                                     PRO20026;
                                                 Human; Interleukin-17 receptor; IL-17RH4; agonist; antagonist; PRO200
DNA 154095-2998; systemic lupus erythematosus; rheumatoid arthritis;
osteoarthritis; diabetes mellitus; allergic disease; asthma;
demyelinating disease; degenerative cartilaginous disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'Glycosaminoglycan attachment site"
                                                                                                                                                                                                                                                                                                                                                                                                                           82. .185
note= "Asn is N-glycosylated"
32. .235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17. .522
note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "N-myristoylation site"
652. .657
                                                                                                                                                                                                                                                                                                                                        "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                         'note= "Asn is N-glycosylated"
.47. .150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  665. .269
note= "Asn is N-glycosylated"
83. .307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132. .437
'note= "N-myristoylation site"
                                                                                                                                                                                                                                 "N-myristoylation site"
                                                                                                                                                                                                                                                                  "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                     "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                            note= "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   707. .712
/note= "N-myristoylation
                  Interleukin 17 receptor, IL-17RH4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Transmembrane
                                                                                                                                                                                                Location/Qualifiers
                                                                                                                         transplantation associated disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000WS-0191007P.
2000WO-US007532.
2000WS-013807P.
2000WS-0213807P.
2000WS-00644848.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US031274.
2000US-0175481P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000WO-US004341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000WO-US005841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128. .433<sup>-</sup>
/note= "N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .424
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                                                                                                                                                                                                                                                                                                                      .6. .59
note= ".
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/note= "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   site"
266.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-MAR-2000;
21-MAR-2000;
21-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-JUN-2000;
22-JUN-2000;
22-AUG-2000;
24-AUG-2000;
                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                         Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-JAN-2000;
                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-DEC-1999;
30-DEC-1999;
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125

9 62

Gaps

14;

122 185 182 232 242 292 302 352 362

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602
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                                                                                                                                                                                                    712
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123 NYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILD 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; interleukin 17; IL-17; IL-17 receptor; angiogenesis; T-lymphocyte proliferation; inflammatory cell infiltration; inmune related disorder; systemic lupus erythematosus; osteoarthritis; rhumatoid arthritis; spondyloarthropathy; systemic solerosis; Sjogren's syndrome; sarcoidosis; autoimmune haemolytic anaemia; thyroiditis; diabetes mellitus; immune-mediated renal disease; demyelinating disease; Guilain-Barre syndrome; hepatobilary disease; hepatitis; inflammatory bowel disease; Whipple's disease; psoriasis; immune-mediated skin disease; erythema multiforme; contact dermatitis; immune-mediated skin disease; erythema multiforme; contact dermatitis; urticaria; immunologic disease of the lung; eosinophilic pneumonia; idiopathic pulmonary fibrosis; transplantation associated disease;
                                                                                                    LSTKYRLAMDNLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNMHQFI
                                                                                    DEEPDWFEKQFVPFHPPPLRYREPVLEKFDSGLVLNDVMCKPGPESDFCLKVEAAVLGAT
                                                                                                                                           GPADSQHESQHGGLDQDGEARPALDGSAALQPLLHTVKAGSPSDMPRDSGIYDSSVPSSE
                                                                                                                                                                   GPADSQHESQHGGLDQDGEARPALDGSAALQPLLHTVKAGSPSDMPRDSGIYDSSVPSSE
                                                                                                                                                                                                    LSLPLMEGLSTDQTETSSLTESVSSSSGLGEEEPPALPSKLLSSGSCKADLGCRSYTDEL
                            LSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNMHQFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human interleukin 17 homologue PRO20026.
                                                                                                                                                                                                                                                                                                                                                                ABU89705 standard; protein; 728 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0113621P.
99WG-US005028.
99US-0131022P.
99US-00311832.
99US-0134287P.
99WG-US010733.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-MAR-2001; 2001US-00816744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          graft-versus-host disease.
                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                               HAVAPL 718
                                                                                                                                                                                                                                                                                          HAVAPL 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2003003546-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                           10-JUL-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JAN-2003
                                                          483
                                                                                                                                                                                                                                                                                                                                                                                              ABU89705;
                                                                                                                                                                                                                                 663
                                                                                                                                                                                                                                                               713
                              473
                                                                                                                                                                         603
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                                                                                                                                                                                                                                                                                           723
                                                                                     533
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                                                                                                                                                                                                                                                                                                                                       RESULT 14
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The invention relates to a nucleic acid having similarity to interleukin-

CC (17.17) or IL-17 receptor comprises at least 80% nucleic acid sequence
identity to a nucleotide sequence which: (a) encodes a polypeptide having
a sequence of appearing as ABUBS697-ABUB9700 and ABUB99702-ABUB99705 (F1-

BB), lacking or having its associated signal peptide; (b) encodes an

EXTRACELIULAR domain of F1-P8 lacking its associated signal peptide; (c)

CONSISTS of a sequence of appearing as ACAB9850-ACAB89853 and ACA89855-

CC ACAB9858687; or (d) consists of the full-length coding sequence of

SC ACAB9858687; or (d) consists of the full-length coding sequence of

CC ACAB9858687; or (d) consists of the full-length coding sequence of

SC ACAB9858687; or (d) consists of the full-length coding sequence of

CC CONSISTS or (d) consists of the full-length coding sequence of

SC ACAB9858687; or (d) consists of the full-length coding sequence of

CC CONSISTS or (d) consists of the full-length coding sequence of

SC ACAB9858687; or (d) consists of the full-length coding sequence of

CC CONSISTS or (d) consists or (d) codes or (d) 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, a transplantation associated disease, graft rejection or graft-versus-host disease. The present sequence represents an IL17 or IL17 receptor homologue of the invention
                                                                                                                                                                                                                                                                                                                                                                     interleukin-17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                               Grimaldi C;
                                                                                                                                                                                                                                                                                                                                                                   New PRO polypeptides and polynucleotides homologous to interleukinuseful for treating e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, or systemic
                                                                                                                                                                                                                   s, Goddard A, Godowski P, Grimaldi
Tumas D, Vanlookeren M, Vandlen R;
od WI, Yansura D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 3703; DB 6;
Pred. No. 0;
2; Mismatches 8;
                                                                                                                                                                                                                                      Hillan K, Tumas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 10; Fig 18; 129pp; English.
                                                                                                                                                                                                                                    Fong S,
                                                 2000US-0244072P.
2000WO-US030873.
2000US-0253646P.
2000WO-US032678.
2000WO-US034956.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96.7%;
              2000WO-US023328.
2000US-0242837P.
                                                                                                                                                     2001WO-US006520
                                                                                                                                                                                                                                                      Li H, Hillan K
Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 96.7
Matches 702, Conservative
                                                                                                                                                                                          (GETH ) GENENTECH INC.
                                                                                                                                                                                                                               Filvaroff E,
                                                                                                                                                                                                                                                                                                              WPI; 2003-428843/40.
                                                                                                                                                                                                                                                                                                                                N-PSDB; ACA89858
                                                     26-OCT-2000;
10-NOV-2000;
                                                                                          28-NOV-2000;
01-DEC-2000;
                                                                                                                                                     28-FEB-2001;
                24-AUG-2000;
24-OCT-2000;
                                                                                                                                   20-DEC-2000;
                                                                                                                                                                                                                                                      Gurney A, L
Watanabe C,
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99US-0138387P 99US-0172096P. 2000US-0175481P. 2000WO-US004341

09-JUN-1999; 23-DEC-1999;

14-MAY-1999;

99WO-US031274

11-JAN-2000;

2000WO-US005601 2000WO-US005841 2000US-0191007P 2000WO-US015264 2000WO-US007532

02-JUN-2000;

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SQPFLNMKFETDYFVKVVPPPSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKPRNLN 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACHDOVAVTILMSPGALGIEFLKGFRVILLEELKSEGRQCQQLILKDPKQLNSSFKRTGME 122
                                                                                                                                           232
                                                                                                                                                        ETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 292
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                                                                                                                                                                                                                                       ATLFTVMCRKKQQENIYSHLDEESSESSTYTAALPRERLRPRPKVFLCYSSKDGQNHMNV 352
                                                                                                                                                                                                                                                     VOCFAYFLODFCGCEVALDLWEDFSLCREGOREWVIQKIHESOFIIVVCSKGMKYFVDKK 412
                                                                                                                                                                                                                                                                                                                                     NYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILD 472
                                                                                                                                                                                                                                                                                                                                                                                     LSTKYRLMDNIPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNMHQFI 532
                                                                                                                                                                                                                                                                                                                                                                                                          LSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNMHQFI 542
                                                                                                                                                                                                                                                                                                                                                                                                                                   DEEPDWFEKQFVPFHPPPLRYREPVLEKFDSGLVINDVMCKPGPESDFCLKVEAAVLGAT 592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSLPLMEGLSTDQTETSSLTESVSSSSGLGEERPPALPSKLLSSGSCKADLGCRSYTDEL 712
                                                                                            SQPFLNMKFETDYFVKVVPFPSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKPRNLN 185
                                                                                                                                                                                                                                                                                                            VOCFAYFLODFCGCEVALDLWEDFSLCREGOREWVIOKIHESOFIIVVCSKGMKYFVDKK 422
                                                                                                                                                                                                                                                                                                                                                             NYKHKGGGRGSGKGELFLVAVSALAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILD 482
                  62
                                                                                                                                                                                                       EMTSCLLONVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF
                                              ACHDOVAVIIIWSPGALGIEFLKGFRVILEELKSEGROCOOLILKDPKOLNSSFKRTGME
                                                                                                                                           ISQ-------HGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTT
                     3 RASASGVPALFVSGEQGVGPASRNSGLYNITRKYDNCTTYLNPVGKHVIADAQNITISQY
RMKAAARPRLCVANE-GVGPASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNITISQY
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transplantation-associated disease; graft-versus-host disease
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2000US-00644848.
2000WO-US023328.
                                                                                                                2000WO-US030873.
2000US-0253646P.
                                                          99WO-US031274.
2000US-0175481P.
2000WO-US004341.
                                                                               2000US-0191007P
                                                                                   2000WO-US007532.
2000WO-US015264.
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                                                                                                                          2000WO-US032678
                                       20-DEC-2000; 2000US-00747259
                                                                         2000WO-US005841
                    US2003008815-A1.
           Homo sapiens.
                                                                                             20-JUN-2000;
                                                                                                                 10-NOV-2000;
28-NOV-2000;
                                                                               21-MAR-2000;
                                                                                   21-MAR-2000;
02-JUN-2000;
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                                                                                                            24-OCT-2000;
                                                                         02-MAR-2000;
                                                 14-MAY-1999
23-DEC-1999
                                                               11-JAN-2000
                                                           30-DEC-1999
                              09-JAN-2003
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(GETH) GENENTECH INC.

ວັ , Grimaldi Vandlen R; Goddard A, Godowski PJ, umas D, Vanlookeren M, V Chen J, Filvaroff E, Fong S, Goddard A, Godov Gurney AL, Li H, Hillan K, Tumas D, Vanlooke: Watanabe C, Williams PM, Wood WI, Yansura DG;

WPI; 2003-341350/32. N-PSDB; ACA64642.

and gene New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO1031, PRO1122, PRO10272, useful in molecular biology, chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy.

Claim 10; Fig 18; 148pp; English.

The invention relates to an isolated nucleic acid comprising at least 80% sequence identity to 8 cDNA sequences encoding PRO polypeptides (or their extracellular domains) which are members of the interleukin-17 (IL-17) family of cytokines. Also included are expression vectors, host cells, the propertides fused to a heterologous amino acid sequence, an anti-PRO antibody, a composition comprising the above polypeptide (or its agonist or antagonist, or the antibody cited above) in combination with a carrier, determining the presence of a PRO polypeptide (or its agonist or antagonist, or the antibody cited above) in combination with a carrier, determining the presence of a PRO polypeptide in a sample, identifying a compound that minics or inhibitis the expression of compound that minics a carrier, identifying a compound that minics in the expression of gene encoding the above polypeptides, etimulating or inhibiting the expression of gene encoding the above polypeptides, etimulating or inhibiting or inhibiting or inflammatory calls into a tissue of a mammal and inhibiting or stimulating angiogenesis induced by a PRO1031 polypeptide or its agonist or in a mammal. The nucleic acid is useful in molecular biology, e.g. use as the proparing PRO polypeptides by recombinant techniques, and in generating either transgenic animals or knock-out animals which, in turn, are useful in the development and screening of therapeutically useful cagnetic ament for treating a condition responsive to the polypeptide or antibody, and in various diagnostic assays. For immune-related disorders, these may be systemic lupus erythematosus, rhemmatosid arthritis, and in various diagnostic assays. For immune-related disorders, these may be systemic lupus erythematosus, rhemmatosid arthritis, and and any despression of a medicament for treating a condition responsive to the polypeptide or the antibody, and such arthritis and any despression of a medicament for treating a condition responsive to the polypeptide or the antibody and arthritis and a ostecarthritis, juvenile chronic arthritis, spondyloarthropathy, systemic sclerosis, idiopathic inflammatory myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating disease of the central or peripheral nervous system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,

Human; interleukin-17; IL-17; cytokine; T-lymphocyte; inflammatory cell; angiogenesis; gene therapy; immune-related disorder; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; systemic sclerosis; idiopathic inflammatory myopathy; Sjogren's syndrome; sarcoidosis; autoimmune haemolytic anaemia; thyroiditis; psoriasis; diabetes mellitus; demyelinating disease; Guillain-Barre syndrome; autoimmune chronic active hepatitis; primary billary cirrhosis; inflammatory bowel disease; immune-mediated skin disease; contact dermatitis; allergic disease; asthma; urticaria; contact dermatitis; allergic disease; asthma; urticaria;

Human IL-17 family member, PRO20026.

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infectious or autoimmuse drands active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease, gluten-ensitive enteropathy, Whipple's disease, autoimmune or immune-mediated skin disease, bullous skin disease, erythema multiforme, contact dermatitis, psoriasis, allergic disease, asthma, allergic rhintis, atopic dermatitis, food hypersensitivity, urticaria, immunologic disease of the lung, eosinophilic pneumonias, indiopathic pulmonary fibrosis, hypersensitivity pneumonitis, transplantation associated disease, graft rejection or graft-versus-host disease. The composition is useful in treating the above-mentioned immune-related diseases in a mammal, or in increasing or inhibiting the proliferation of Inflammatory cells into a tissue of a mammal. The present sequence represents a PRO polypeptide of the invention
polyneuropathy, hepatobiliary disease.
        inflammatory demyelinating
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Sequence 728 AA;

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|SQHGSDMQVSFDHAPHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTT
                                                                                                                                                                                                                                                                                                                                                        ATLFTVMCRKKQQENIYSHLDEESSBSSTYTAALPRERLRPRPKVFLCYSSKDGQNHMNV
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                                                                   7 RMKAAARPRLCVANE-GVGPASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNITISQY
                                                                                      SQPFILNMKFETDYFVKVVPFPSIKNESNYHPFFFRTRACDLLLQPDNIACKPFWKPRNLN
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                                    Gaps
                                    14;
96.7%; Score 3703; DB 6; Length 728; 96.7%; Pred. No. 0; ive 2; Mismatches 8; Indels 1.
                    Best Local Similarity 96.7
Matches 702; Conservative
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HAVAPL 728

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RESULT 1
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                                                                   August 9, 2005, 11:38:07; Search time 29.2862 Seconds (without alignments) 1830.146 Million cell updates/sec
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Sequence 12, Ap
Sequence 12, Ap
Sequence 11658,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10,
                                                                                                                                         ....CKADLGCRSYTDELHAVAPL 718
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/cgn2_6/ptodata/1/jaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-949-016-8005
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US-09-022-255-10

US-09-022-253-10

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US-09-022-259-10

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US-09-816-744-12
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28 113.5 3.0 617 4 US-09-312-283C-303 Sequence 303, App 29 112.5 2.9 549 4 US-09-949-016-6384 Sequence 5384, Ap 30 111.5 2.9 489 4 US-09-248-796A-25826 Sequence 1, Appli 31 110.5 2.9 993 1 US-08-348-143-1 Sequence 1, Appli 33 110.5 2.9 993 3 US-09-192-435-1 Sequence 1, Appli 34 110.5 2.9 993 4 US-09-192-435-1 Sequence 1, Appli 35 110.5 2.9 993 4 US-09-192-435-1 Sequence 1, Appli 36 109 2.8 998 2 US-08-45A-20 Sequence 20, Appli 37 109 2.8 998 5 PCT-US5-04681-20 Sequence 20, Appli 39 102 2.7 838 4 US-09-949-016-9916 Sequence 20, Appli 39 102 2.7 838 4 US-09-949-016-9917 Sequence 20, Appli 40 101 2.6 990 4 US-09-949-016-9917 Sequence 10562, Appli 40 100 2.6 619 4 US-09-949-016-1449 Sequence 10562, Appli 40 100 2.6 595 2 US-08-36-443-6 Sequence 3, Appli 40 100 2.6 595 2 US-08-36-843-3 Sequence 664, Appli 40 100 2.6 595 2 US-08-36-843-3 Sequence 3, Appli 40 100 2.6 595 2 US-08-36-843-3 Sequence 664, Appli 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.0 50 2.
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Best Local Similarity 96.7%; Pred. No. 0;
Matches 702; Conservative 2; Mismatches
PRIOR APPLICATION NUMBER: US 60/242,837
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: PCT/US00/30873
PRIOR FILING DATE: 2000-11-10
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/253,646
PRIOR PLING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR PILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 39
                                                                                                                       TYPE: PRT
ORGANISM: Homo Sapien
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, Williams, P. Mickey
APPLICANT: Wood, Williams
APPLICANT: Yansura, Daniel
TITLE OF INVENTION: IL-17 HOWOLOGOUS POLYPEPTIDES
FILE REPERENCE: P1381R1C1P2 (US)
CURRENT APPLICATION NUMBER: US/09/816,744
CURRENT FILING DATE: 2001-03-22
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llarity 96.7%; Pred. No. 0;
Conservative 2; Mismatches
Sequence 18, Application US/09816744 Patent No. 6579520 GENERAL INFORMATION:
                                                                                                                    Godowski, Paul
Grimaldi, Christopher
Gurney, Austin
                                                                                                                                                                                                                       VanLookeren, Menno
Vandlen, Richard
                                                                                                                                                                    Li, Hanzhong
Hillan, Kenneth
Tumas, Daniel
                                                     APPLICANT: Chen, Jian
APPLICANT: Filvaroff, Ellen
                                                                                      Fong, Sherman
Goddard, Audrey
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ORGANISM: Homo Sapien
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Best Local Similarity
Matches 702; Conserv
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                                 100 LQTDASILYLEGAELSVLQLNTNERLCVR--FBFLSKLRHHHRRWRFTFSHFV-VDPDQE 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : | | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
79 -PGALGIEFLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFKRTGMESQPFLNMKFETD 137
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Patent No. 6072033
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INFORTION: No. 6072033el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDERSS:
ADDRESSEB: Immunex Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            657 LMEGLSTDQTETSSLTESVSSSGLGEEEPPALPSKLLSSGSCKADLGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  566 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHE----
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Apple Power Macintosh
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MEDIUM TYPE: Floppy (COMPUTER: Apple Powe)
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                                                                                                                                                                                                                                     LSLPLMEGLSTDQTETSSLTESVSSSSGLGEEEPPALPSKLLSSGSCKADLGCRSYTDEL 712
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8.1%; Score 312; DB 2; Length 866;
Best Local Similarity 23.1%; Pred. No. 1.4e-23;
Matches 178; Conservative 107; Mismatches 338; Indels 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
CORRESPONDENCE ADDRESS:
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CONDITION TITE: TOPPY THEN COMPUTER:

SOFTHARE: MICROSOFT WORD FOR APPLE, Version 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/620,694A

FILING DATE: 21 MARCH 1996

CLASSIFICATION DATA:

APPLICATION NUMBER: US/N 08/538,765

FILING DATE: 7 AUGUST 1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/N 08/410,535

FILING DATE: 23 MARCH 1995

CLASSIFICATION: 435

PRIOR APPLICATION: 435

PRIOR APPLICATION: 435

PRIOR APPLICATION: 435

PRIOR APPLICATION: 435

ATONNEY/AGENT INFORMATION:

NAME: PERKINS, PALTICIA ANDE

REGISTRATION NUMBER: 34,695

REGISTRATION NUMBER: 34,695

REGISTRATION NUMBER: 2617-B

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
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MOLECULE TYPE: protein
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100 LQTDASILYLEGABLSVLQLNTNERLCVR--FEFLSKLRHHHRRWRFTFSHFV-VDPDQE 156
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606 IDQDGEARPALDGSA---ALQ-----PLLHTVKAGSPSDMPRDSGIYDSSVPSSELSLP 656
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                                             677 LVAAVEPGPLADGAAVRLALAGEGEACPLLGSPGAG-----RNSVLF---LPVDPEDSP
                                                                                                                                     L--GSSTPMASPDLLPEDVR-----EHLEGLMLSLFEQSLSCQAQGGC 768
                                                                                                                                                                                                                                                                                                                                          APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Spriggs, Milliam
APPLICANT: Panslow, William
TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
UNMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.1%; Score 312; DB 3; Length 866; 23.1%; Pred. No. 1.4e-23;
                                                                                               657 LMEGLSTDQTETSSLTESVSSSGLGEEEPPALPSKLLSSGSCKADLGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 338;
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                                                                                                                                                                                                                                                                Sequence 10, Application US/09022696; Patent No. 6072037; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 261
TELECOMMINICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 23.1%; ri
Matches 178; Conservative 107;
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FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
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PRIOR APPLICATION DATA:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RSKSGRSLYVAICNMHQFIDEEPDWFE-----KQFVPFHPPPLRYREPVLEKFDSGL 565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138 YFVKV--VPFPSIKNESNYHPFFFRTRACDLLLQPDNLACK---PFWKPRNL----- 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157 YEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHARMKVTTPCMSSGSLWDP-NITVETLEAH 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----NISQHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTETT 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 NITEKYDNC--TTYLNPVGKHVIADAQNIT-----ISQYACHDQ-----VAVTILWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 338; Indels 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 866;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.1%; Score 312; DB 3;
llarity 23.1%; Pred. No. 1.4e-23;
Conservative 107; Mismatches 338;
                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/620,694
FILING DATE: 21 MARCH 1996
APPLICATION NUMBER: USSN 08/518,765
FILING DATE: 7 AUGUST 1995
PRIOR APPLICATION DATA: SPELICATION DATA: SPELICATION DATA: SPELICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION PROMISE: 23 MARCH 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                      NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REPERENCE/DOCKET NUMBER: 2617-B
TELECOMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                          10:
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SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYPE: amino acid
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178; Conserv
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Best Local S
Matches 178
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REFERENCE/DOCKET NUMBER:
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US-08-978-773-4
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                                                                                                                                                                                                                                                                                                                                                      RSKSGRSLYVAICNMHQFIDEEPDWFE-----KQFVPFHPPPLRYREPVLEKFDSGL 565
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                                                                                              GCCRHQVQIQPFFSSCLNDCLRHSATVSCPEMPDTPEPIPDYMPLWVWFITGISILLVG 334
                                                                                                                             ATLFTVMCRKKQOENIYSHLDEESSESTYTAALPRERLRPRP----KVFLCYSSKDGQN 348
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                                                                                                                                                                                                                                                                    TR----AKWQALLGRGAPVRLRCDHGKPVGDLFTAAMNMILPDFKR-----PACFGTYVV 501
                                                                                                                                                                                                                                                                                                                                                                                                            509 BBHÖS-----
                 -----NISQHGSDMQVSFDHAPHNFGFRPYLHYKLKHEGPFKRKTCKQEQTTETT 235
                                     216 QLRVSFTLWNBSTHYQILLTSFPHMENHSCFEHMH-HIPAPRPEBFHQRSNVTLTLRNLK 274
                                                                      SCLLONVSPGDYIIELVDDT---NTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 292
                                                                                                                                                                                                                                                                                                               502 CYFSEVSCDGDVPDLFGAAPRYPLMDRFEEV--YFRIQDLEMFQPGRMHRVGELSGDNYL
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APPLICANT: Troutt, Anthony
TITLE OF INVENTION: Method of Regulating Nitric Oxide Production
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          657 LMEGLSTDQTETSSLTESVSSSGLGEREPPALPSKLLSSGSCKADLGC 705
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple PowerMacintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for PowerMacintosh, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,773
                                                                                                                                                                                                                                                                                                                                                                                                               VINDVMCKPGPESDFCLKVEAAVLGATGPADSQHE-----
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/052,525
FILING DATE: 27 NOVEMBER 1996
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 51 University Street CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08978773
Patent No. 6083906
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NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVILLIVCMTWRLAGPGS---EKYSDDTKYTDGLPAADLIPPPLKPRKVWIIYSA-DHPL 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   349 HMNVVQCPAYFLQDFCGCBVALDLWEDFSLCREGQREWV----IQKIHESQFIIVVCSKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VYF-DYSCEGDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTRQG--SRRNYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 NITFKYDNC--TTYLNPVGKHVIADAQNIT-----ISQYACHDQ-----VAVTILWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138 YFVKV--VPFPSIKNESNYHPFFFRTRACDLLLQPDNLACK---PFWKPRNL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----NISQHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RSKSGRSLYVAICNMHQFIDEEPDWFE-----KQFVPFHPPPLRYREPVLEKFDSGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LMEGLSTDQTETSSLTESVSSSGLGEEFPPALPSKLLSSGSCKADLGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L--GSSTPMASPDLLPEDVR-----EHLEGLMLSLFEQSLSCOAQGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 866;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 8.1%; Score 312; DB 3; Length 86
Best Local Similarity 23.1%; Pred. No. 1.4e-23;
Matches 178; Conservative 107; Mismatches 338; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10, Application US/09022253
Patent No. 6096305
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 587-0430
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: almo acid
TYPE: Almo acid
TYPE: Almo acid
TYPE: Almo acid
TYPE: Almo acid
TYPE: Almo acid
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335 SVILLIVCMTWRLAGPGS---EKYSDDTKYTDGLPAADLIPPPLKPRKVWIIYSA-DHPL 390
                                                                                                                                                                                                         405 MKYFVDKKONYKHKGGG-----RGSGKGELFLVAVSAIAEKLROAKOSSSAALSKFIA 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----SQHGG 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LDQDGEARPALDGSA---ALQ----PLLHTVKAGSPSDMPRDSGIYDSSVPSSELSLP 656
                                                                    349 HMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWV----IQKIHESQFIIVVCSKG 404
                                                                                                                                                                                                                                                                             451 TR----AKWQALLGRGAPVRLRCDHGKPVGDLFTAAMMILPDFKR-----PACFGTYVV 501
                                                                                                                                                                                                                                                                                                                                                 457 VYP-DYSCEGDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTRQG--SRRNYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RSKSGRSLYVAICNMHQFIDEEPDWFE-----KQFVPFHPPPLRYREPVLEKFDSGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   657 IMEGLSTDQTETSSLTESVSSSGLGEEEPPALPSKLLSSGSCKADLGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Word for Apple, Version 6.0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           566 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Perkins, Patricia Anne
REGISTRATION UNMBER: 34,695
REPERRUCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
US-09-022-260-10
'Sequence 10, Application US/09022260
'Patent No. 6100235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (206) 587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 LQTDASILYLEGAELSVLQINTNERLCVR--FEFLSKLRHHHRRWRFTFSHFV-VDPDQE 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138 YFVKV--VPFPSIKNESNYHPFFFRTRACDLLLQPDNLACK---PFWKPRNL----- 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157 YEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHARMKVTTPCMSSGSLWDP-NITVETLEAH 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----NISOHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTETT 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        216 QLRVSFTLWNESTHYQILLTSFPHMENHSCFEHMH-HIPAPRPEEFHQRSNVTLTLRNLK 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236 SCLLQNVSPGDYIIELVDDT---NTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         275 GCCRHQVQIQPFFSSCLNDCLRHSATVSCPEMPDTPEPIPDYMPLWVYWFITGISILLVG 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATLFTVMCRKKQQENIYSHLDEESSESTYTAALPRERLRPRP----KVFLCYSSKDGQN 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 NITFKYDNC--TTYLNPVGKHVIADAQNIT-----ISQYACHDQ-----VAVTILWS 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----RNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWT
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                 AREAL INCORPATION.
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
IITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
APPLICATION DATA:
APPLICATION NUMBER: US/09/022,253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 8.1%; Score 312; DB 3;
Best Local Similarity 23.1%; Pred. No. 1.4e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694
FILING DATE: 21-MARCH-1996
FILING DATE: 7 AUGUST 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
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                                                                                                                                                                 NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AFFLIANTON NOTED AT A TAILOR DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 26
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INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (206) 587-0430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: protein US-09-022-253-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                     98101
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                                                                                                                                                                                                                                                                                                                                                 STATE: W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185
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APPLICATION NUMBER: US/09/022,259 FILING DATE:
                                                                                                                                                                                                                                                                     COMPUTER: Apple Power macintosh OPERATING SYSTEM: Apple Operatin SOFTWARE: Microsoft Word for Apr
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REGISTRATION NUMBER: 34,695
REPERENCE/DOCKET NUMBER: 2617-B
TELECOMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                    E: Immunex Corporation
51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-09-022-259-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 LQTDASILYLEGAELSVLQLATNERLCVR--FEFLSKLRHHHRRWRFTFSHFV-VDPDQE 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       157 YEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHARMKVTTPCMSSGSLMDP-NITVETLEAH 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----NISQHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTETT 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216 QLRVSFTLWNESTHYQILLTSFPHMENHSCFEHMH-HIPAPRPEBFHQRSNVTLTLRNLK 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    293 ATLFTVMCRKKQQENIYSHLDEESSESTYTAALPRERLRPRP----KVFLCYSSKDGQN 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVILLIVCMTWRLAGPGS---EKYSDDTKYTDGLPAADLIPPPLKPRKVWIIYSA-DHPL 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :: | :: | :: | :: TR----AKWQALLGRGAPVRLRCDHGKPVGDLFTAAMMMILPDFKR-----PACFGTYVV 501
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                                                                                                                                                                                                                                                                                                                                                                                                                              79 -PGALGIEFLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFKRTGMESQPFLNMKFETD 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YFVKV--VPFPSIKNESNYHPFFFRTRACDLLLQPDNLACK---PFWKPRNL------ 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCLLQNVSPGDYIIELVDDT---NTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HMANVACEAYFLODFCGCEVALDLWEDFSLCREGOREWY----IQKIHESOFIIVVCSKG 404
                                                                                                                                                                                                                                                                                                              34 NITEKYDNC--TTYLNPVGKHVIADAQNIT-----ISQYACHDQ-----VAVTILWS 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VYF-DYSCEGDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTRQG--SRRNYF
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Sequence 10, Application US/09022259

Sequence 10, Application US/09022259

Patent No. 6191104

GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin

APPLICANT: Spriggs, Melanie

APPLICANT: Fandlow, William

TITLE OF INVENTION: No. 6191104el Receptor That Binds IL-17
                                                                                                                                                                                                  8.1%; Score 312; DB 3; Length 866; 3.1%; Pred. No. 1.4e-23;
                                                                                                                                                                                                     Query Match

8.1%; Score 312; UB 3; Length Co. 1.4e-23;
Best Local Similarity 23.1%; Pred. No. 1.4e-23;
Matches 178; Conservative 107; Mismatches 338; Indels
     SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYPE: amino acid
                                                                                     TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-022-260-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCLLQNVSPGDYIIELVDDT---NTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         275 GCCRHQVQIQPFFSSCINDCLRHSATVSCPEMPDTPEPIPDYMPLWYWFITGISILLVG 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                293 ATLFTVMCRKKQQENIYSHLDEESSESSTYTAALPRERLRPRP----KVFLCYSSKDGQN 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SVILLIVCMTWRLAGPGS---EKYSDDTKYTDGLPADLIPPPLKPRKVWIIYSA-DHPL 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MKYFVDKKNYKHKGGG------RGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIA 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79 - PGALGIEFLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFKRTGMESQPFLNMKFETD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216 QLRVSFTLWNESTHYQILLTSPPHMENHSCFEHMH-HIPAPRPEEFHQRSNVTLTLRNLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWV----IQKIHESQFIIVVCSKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 NITPKYDNC--TTYLNPVGKHVIADAQNIT-----ISQYACHDQ-----VAVTILWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157 YEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHARMKVTTPCMSSGSLWDP-NITVETLEAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138 YFVKV--VPFPSIKNESNYHPFFFRTRACDLLLQPDNLACK---PFWKPRNL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
8.1%; Score 312; DB 3; Length 866;
Best Local Similarity 23.1%; Pred. No. 1.4e-23;
Matches 178; Conservative 107; Mismatches 338; Indels 146;
SYSTEM: Apple Operating System 7.5.5 Microsoft Word for Apple, Version 6.0.1
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                                                                                                                                         RSKSGRSLYVAICNMHQFIDEEPDWFE-----KQFVPFHPPPLRYREPVLEKFDSGL 565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LDQDGEARPALDGSA---ALQ----PLLHTVKAGSPSDMPRDSGIYDSSVPSSELSLP 656
L--GSSTPMASPDLLPEDVR-----EHLEGLMLSLFEQSLSCQAQGGC 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Spriggs, Milliam
TITLE OF INVENTION: No. 6197525el Receptor That Binds IL-17
CORRESPONDENCE: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LMEGLSTDQTETSSLTESVSSSSGLGEEEPPALPSKLLSSGSCKADLGC
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OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,257
                                                                                                                                                                                                                                                                                                                                                         VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHE----
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PRIOR APPLICATION DATA:
PAPPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 23 MARCH 1995
CLASSIFICATION INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Parricia Anne
REGISTRATION NUMBER: 34,695
REGISTRATION NUMBER: 34,695
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/09022257
Patent No. 6197525
GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
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US-09-022-257-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----NISQHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTETT 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 : : | | : : | | : : | | : : | | : : | | : : : | | : : : | | : : : | | : : : : | | : : : : | | : : : : | | : : : | | : : : : | | : : : | | : : : | | : : : | | : : : : | | : : : : | | : : : : | | : : : : | | : : : : | | : : : : | | : : : : | | : : : : | | : : : : | | : : : : | | : : : : | | : : : : | | : : : : | | : : : : | | : : : : | | : : : : | | : : : : | | : : : : | | : : : : | | : : : : | | : : : : | | : : : : | | : : : : | | : : : : | | : : : : | | : : : : | | : : : : | | : : : : | | : : : : | | : : : | | : : : : | | : : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       349 HMAVVQCFAYFLQDFCGCEVALDLWEDFSLCREGOREWV----IQKIHESQFIIVVCSKG 404
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                                                                                                                                                                                                                                                                                  34 NITEKYDNC--TTYLNPVGKHVIADAQNIT-----ISQYACHDQ-----VAVTILWS
     Query Match 8.1%; Score 312; DB 3; Length 866;
Best Local Similarity 23.1%; Pred. No. 1.4e-23;
Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps
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Spriggs, Melanie
Spriggs, Melanie
Faralow, William
TITLE OF INVENTION: No. 6680057el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
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Length 866;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
US-09-549-679-10
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676 959 727

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APPLICANT: WOHLER, Kendall M.
TITLE OF INVENTION: Methods for Treating Rheumatoid Arthritis Using IL-17 Antagonists
FILE REPERBERS: 2982-2001-10-18
CURRENT APPLICATION NUMBER: US/10/033,522
CURRENT FILING DATE: 2001-10-18
PRIOR APPLICATION NUMBER: US 60/241,230
PRIOR FILING DATE: 2000-10-18
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 -PGALGIEFLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFKRTGMESQPFLNMKFETD 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157 YEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHARMKVTTPCMSSGSLWDP-NITVETLEAH 215
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                                                               -----NISQHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTETT
                                                                                                                  LDQDGEARPALDGSA---ALQ-----PLLHTVKAGSPSDMPRDSGIYDSSVPSSELSLP
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NCTVKNSTCLDDSWIHP-----RNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138 YFVKV---VPFPSIKNESNYHPFFFRTRACDLLLQPDNLACK---PFWKPRNL----
560 RSPGGRQLRAALDRFRDWQVRCPDWFECENLYSADDQDAPSLDEEV-FEEPLLPP-GTGI
                                      -SOHGG
                                                                                                                                                                                             705
                                                                                                                                                                                                                               L--GSSTPMASPDLLPEDVR----EHLEGLMLSLFEQSLSCQAQGGC 768
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                                                                                                                                                                                             LMEGLSTDQTETSSLTESVSSSGLGEEEPPALPSKLLSSGSCKADLGC
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23.1%; Pred. No. 1.4e-23;
ive 107; Mismatches 338;
                                      VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHE ---
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Patent No. 6793919
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Matches 178; Conservative 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn version 3.1 SEQ ID NO 1
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US-10-033-522-1
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                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
                                                                                                                                                          FILING DATE: 14-Apr-2000
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE: <UNKNOWN>
APPLICATION WHOBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                        APPLICATION NUMBER: US/09/549,679
                                                                                                                                                                                                                                                                                                                 NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFRERNCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYPE: amino acid
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342 IICMTWRLSGADQEKHGDDSKINGILPVADLTPPPLRPR-KVWIVYSA-DHPLYVEVVLK 399
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                                                                                                                                                                                                                                                                      132 ISMIQHHRKRWRFSF----SHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKIIFVPDC 185
                                                                                                                                                                                                                                                                                                                                                                      :: :: :: | | | :: : | | | 1.85 EDSKYMKWITSCVSSGSLWDP-NITVETLDTQHLRVDFTLWNESTPYQVLLESFSDSENHS 244
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                                                                                                                                 --LILKDPKQLNSSFKRTGMESQPFLNMKFETDYFVKVVPFPSIKNESNYHPFFFRTRAC 164
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----MEGLSTDQTETSSLTESVSSSGLGEEEPP-----ALPSKLLSSGSCKADLG
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                                                                                         HVIADAQNITISQYACHDQVAVT-ILWS-PGALGIEFLKGFRVILEELKSEGRQCQQ---
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Patent No. 6072033
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Panslow, William
TITLE OF INVENTION: No. 6072033e1
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
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COUNTRY: US
ZIP: 98101
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US-09-022-255-2
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618 VKRAPLVRE-PGSQACLAIDPLVGEEGGAAVAKLEPHLQPRGQPAPQPLHTLVLAAEEGA 676
                                                                    RSKSGRSLYVAICNMHQFIDEEPDWFE-----KQFVPFHPPPLRYREPVLEKFDSGL 565
                                                                                                                                                                                      566 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHE------SQHGG 605
                                                                                                                                                                                                                                                                                                            LDQDGEARPALDGSA---ALQ-----PLLHTVKAGSPSDMPRDSGIYDSSVPSSELSLP 656
                                                                                                                                                                                                                                                                                                                                                                   677 LVAAVEPGPLADGAAVRLALAGEGEACPLLGSPGAG-----RNSVLF---LPVDPEDSP 727
         502 CYPSEVSCDGDVPDLFGAAPRYPLMDRFEEV--YFRIQDLEMFQPGRMHRVGELSGDNYL 559
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22.5%; Pred. No. 6.1e-23;
tive 129; Mismatches 320; Indels 202;
                                                                                                                                                                                                                                                                                                                                                                                                                              705
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Patent No. 5869286
GENERAL INFORMATION:
APPLICANT: Yoro, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION:
NO. 5869286el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
COMPUTER: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694A
FILLING DATE: 21 MARCH 1996
CLASSIFICATION: 435
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILLING DATE: 23 MARCH 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
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APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
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STREET: 51 University Street
CITY: Seattle
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(206)
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TYPE: amino acid
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MOLECULE TYPE: protein
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Best Local Similarity
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US-08-620-694A-2
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STATE:
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TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 587-0430
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US-09-022-696-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D---LLLLQPDNLACKPFWKPRNLNI----SQH--------GSDMQV 195
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          MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/022,255
                                                                                                                                     FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/620,694
FILING DATE: 21 MARCH 1996
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
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SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
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MOLECULE TYPE: protein
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09022696

Sequence 2, Application US/09022696

Patent No. 6072037

GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Panishow, William
TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
COMPATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,696
                                                                                                                                                                                    572 CKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQD--
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STREET: 51 University Street
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE:
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REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/.
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
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Search completed: August 9, 2005, 11:51:19 Job time : 40.2862 secs

Perfect score:

Sequence:

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Searched:

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Sequence 13, Appl
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Sequence 84, Appl
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Sequence 26425, P
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Fatent No. US20020165348A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kuestner, Rolf E.
APPLICANT: Gao, Zeren
TITLE OF INFORMATION: Human Cytokine Receptor
FILE REFERENCE: 00-49
CURRENT APPLICATION NUMBER: US/09/912,157
CURRENT FILING DATE: 2001-07-23
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 3.0
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0; Mismatches
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Matches 2383, Conservative
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; LOCATION: (86)...(2344)
US-09-912-157-1
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ORGANISM: Homo sapiens
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| cgn2 6/ptodata/2/pubpna/USO6_PUBCOMB. seq:*
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| cgn2 6/ptodata/2/pubpna/USO8 PUBCOMB. seq:*
| cgn2 6/ptodata/2/pubpna/USO9 PUBCOMB. seq:*
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                                                                                                                                                                           Sequence 1, Application US/10717282
; Sequence 1, Application US/10717282
; Publication No. US20040077052A1
; GENERAL INFORMATION:
   APPLICANT: Presnell, Scott R.
   APPLICANT: Gao, Zeren
   TITLE OF INVENTION: Human Cytokine Receptor
   FILE REFERENCE: 00-49
   CURRENT APPLICATION NUMBER: US/10/717,282
   CURRENT PILING DATE: 2003-11-19
   PRIOR APPLICATION NUMBER: US/09/912,157
   PRIOR PILING DATE: 2001-07-24
   NUMBER OF SEQ ID NOS: 13
   SOFTWARE: FastSEQ for Windows Version 3.0
   SEQ ID NO 1
   LENGTH: 2383
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100.0%; Score 2383;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2383; Conservative 0; Mismatches
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99.7%; Score 2376.6;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2379; Conservative 0; Mismatches
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (86)...(2344)
   ; ORGANISM: Hom
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APPLICANT: Kuestner, Rolf E.
APPLICANT: Gao, Zeren
TILE OF INVENTION: Human Cytokine Receptor
FILE REFERENCE: 00-49
CURRENT APPLICATION NUMBER: US/09/912,157
CURRENT FILING DATE: 2001-07-23
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 4
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Patent No. US20020165348A1
GENERAL INFORMATION:
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LENGTH: 2383
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      APPLICANT: Presnell, Scott R.
APPLICANT: Kuestner, Rolf E.
APPLICANT: Goo, Zeren
TITLE OP INVENTION: Human Cytokine Receptor
FILE REPERRNCE: 00-49
CURRENT APPLICATION NUMBER: US/09/912,157
CURRENT FILING DATE: 2001-07-23
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 7
LENGTH: 2341
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US-09-912-157-7
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Publication No. US20040077052A1

GENERAL INPORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: Presnell, Scott E.
APPLICANT: Gao, Zeren
ITLE OF INVENTION: Human Cytokine Receptor
FILE REFERENCE: 00-49
CURRENT APPLICATION NUMBER: US/10/717,282
CURRENT APPLICATION NUMBER: US/09/912,157
PRIOR APPLICATION NUMBER: US/09/912,157
PRIOR APPLICATION NUMBER: US/09/912,157
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
LENGTH: 2341
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Best Local Similarity 98.2%;
Matches 2341; Conservative C
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US-10-717-282-7
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Qy 2281 GTCATGCAAAGCAGATCTTGGTTGCCGCAGCTACACTGATGAACTCCACGCGGTCGCCCC 2340 Db 2239 GTCATGCAAAGCAGATCTTGGTTGCCGCAGCTACACTGATGAACTCCACGCGGTCGCCCC 2298 Qy 2341 TTTGTAACAAAACGAAAGATCTAAGCATTGCCACTTTAGCTG 2383 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	RESULT 7 US-10-842-006-1 i Sequence 1, Application US/10842006 j Publication No. US20040235104A1 j GENERAL INFORMATION: ADPLICANTY YANG RUEY-BING	; TITLE OF INVENTION: A NOVEL Human SEF Molecule and Uses; TITLE OF INVENTION: Therefor; FILE REFRENCE: MP103-071PIPM ; CURRENT APPLICATION NUMBER: US/10/842,006 ; CURRENT FILIG DATE: 2004-05-07	; FALON AFPLICATION NOBER: 00/403522; PALON FILING DATE: 2003-05-08; NUMBER OF SEQ ID NOS: 12; SOFFWARE: FastSEQ for Windows Version 4.0	; SEQ II NO I ; TYPE: DNA ; ORGANISM: Homo Sapiens	; TANK KEY: CDS ; LOCATION: (90)(2309) US-10-842-006-1	Query Match 95.8%; Score 2282.6; DB 20; Length 4477; Best Local Similarity 98.1%; Pred. No. 0; Matches 2337; Conservative 0; Mismatches 4; Indels 42; Gaps 1.	Oy 1 CCGCCGCGCCCACTCGGGGCTGGCCGGGCGGCGGCGGCGGCGGCGCAGAAAC 60	Oy 61 GGCCTGGCTGGCGAGGCAAGGCCATGGCCCGTGGCTGCAGCTCTGCTCCTCTT 120	Oy 121 TACGGTCAACGCCTGCACCAACGGCTCGCAGCTGGCCGCTGGCGGGGGGGCCGCTGGCCGCCG 180	OY 181 CGCGCGGGCGCCGA.CTCTGGCTGGAGGATGAAAGCGGCTGCCCCGACCCCGGCTTTG 240	Oy 241 IGTIGCTAATGAGGAGCCAGCCAGCAGAAACAGTGGGCTGTACAACATCACCTT 300	OY 301 CAAATATGACAATTGTACCACTTGAATCCAGTGGGGAAGCATGTGATGCTGACGC 360	OY 361 CCAGAATATCACCATCAGCCAGTATGCTTGCCATGACCAGTGGCAGTCACCATTTTG 420	OY 421 GTCCCAGGGGCCCTCGGCATCGAATTCCTGAAAGGATTTCGGGTAATACTGGAGGGT 480	Qy 481 GAAGTCGGAGGGAAGACAGTGCCAACAACTGATTCTAAAGGATCCGAAGCAGCTCAACAG 540
1201 CTTTCTCTGCTATTCCAGTAAGATGGCCAGAATCACATGAATGTCGTCCAGTGTTTCGC	CCTCTGTAGAGAAGGGCAGAGAATGGGTCATCCAGAAGATCCC	1339 CATTGGGTTTGTTGTAAGGTATGAAGTTTGTGGACHAINININININININININININININININININININ	1501 CGAAAAGCTCCGCCAGGCCAAGCAGAGTTCGTCCGCGGCGCTCAGCAAGTTTATCGCCGT 1560 	1561 CTACTTTGATTATTCCTGCGAGGAGGACGTCCCCGGTATCCTAGACCTGAGTACCAGGTA 1620 	1621 CAGACTCATGGACAATCTTCCTCAGCTCTGTTCCCACTTGCACTCCCGAGACCACGGCCT 1680 	1681 CCAGGAGCCGGGGCAGCACAGGGCAGCAGAACTACTTCCGGAGCAAGTC 1740 	1741 AGGCCGGTCCCTATACGTCGCCATTTGCAACATGCACCAGTTTATTGACGAGGAGCCCGA 1800 	1801 CTGGTTCGAAAAGCAGTTCGTTCCTTCCATCCTCCACGCGCTACCGGAGCCAGT 1860 	1861 CTTGGAGAAATTTGATTCGGGCTTGGTTTTAAATGATGTCATGTGCAACCAGGGCCTGA 1920 	1921 GAGTGACTICTGCCTAAAGGTAGAGGGGCTGTICTTGGGGCAACCGGACCAGCCGACTC 1980 	1981 CCAGCACGAGAGTCAGCATGGGGCCTGGACCAAGACGGGGAGGCCCGGCCTGCCCTTGA 2040 	2041 CGGTAGCGCCGCCCTGCAGCCCCTGCTGCACGGTGAAAGCCGGCAGCCCCTCGGACAT 2100 	2101 GCCGCGGGACTCAGGCATCTATGACTCGTCTGTGCCCTCATCCGAGCTGTCTCTGCCACT 2160	2161 GATGGAAGGACTCTGGACGGACCAGAAAGGTCTTCCCTGACGGAGGGGGTGTCCTC 2220 	2221 CTCTTCAGGCCTGGGTGAGGAACCTCCTGCCCTTCCTTCC

1583	Oy 1681 CCAGGAGCCGGGGCACCACCGACAGGAGGAAGGAACTACTTCCGGAGCAAGTC	OY 1741 AGGCCGGTCCTAIACGTCGCCATTTGCAACAIGCACCAGTTTAITGAGAGGCCCGA	1801	1861	1921		2041	2101	2123	2221	2281	DD 2303 TTTGTAACAAAAGGAAGGTCTAAGCATTGCCACTTTAGCTG 2345	RESULT 8 US-10-608-449-1 Sequence 1, Application US/10608449	GENERAL INFORMATION ; APPLICANT: Tsinghua University ; TITLE OF INVENTION: Human Interleukin-17 Receptor Like Molecule ; FILE PEREPRINE. 170013549C-18	CURRENT APPLICATION NUMBER: US/10/608,449 CURRENT FILING DATE: 2003-06-30 NUMBER OF SEQ ID NOS: 19 CONTWADE: DefentIn version 3 1	SEQ ID NO 1 ; LENGTH: 4477 ; TYPE: DNA	9 6066 02000	zo; nengun 4; Indels
541 TAGCTTCAAAAGAACTGGAATGGAATCTCAACCTTTCCTGAATATGAAATTTGAAACGGA 600 	601 TTATTICGTAAAGGTIGTCCCTTTTCCTTCCATTAAAAAGGAAAGCAATTACCACCCTTT 660 	CTTCTTTAGAACCCGAGCCTGTGACCTGTTGTTACAGCCGGACAATCTAGCTTGTAAACC	CTTCTGGAAGCCTCGGAACCTGACCACATCAGCCAGCATGGCTGTCCTT CTTCTGGAAGCCTCGGAACCTGAACATCAGCCACATGGCTGTCTT CTTCTGGAAGCCTCGGAACCTGAACATCAGCACATGGCTCGAACATGCAGGTGTCTT		841 CGAAGGACCTTTCAAGCGAAAGACCTGTAAGCAGGAAGCAAACTACAGAGACGACCAGCTG 900 	901 CCTCCTTCAAAATCTTTCTCCAGGGGATTATAAATTGAGCTGGTGGACACTAACAC 960 	961 AACAAGAAAAGTGATGCATTATGCCTTAAAGCCAGTGCACTCCCCGTGGGCCGGCC	1021 CAGAGCCGTGGCCATCACAGTGCCACTGGTAGTCATATCGGCATTCGCGACGCTCTTCAC 1080	1081 TGTGATGTGCCGCAAGAAGCAACAAGAAATATATATCACATTTAGATGAAGAGCTC 1140 	1141 TGAGTCTTCCACATACACTGCAGCACTCCCAAGAGAGAGCTCCGGCGCGCGC	1201 CTTTCTCTGCTATTCCAGTAAAGATGGCCAGAATCACATGAATGTCGTCCAGTGTTTCGC 1260 	1261 CTACTICCTCCAGGACTICTGTGGCTGTGAGGTGGCTCTGGACCTGTGGGGAAGACTTCAG 1320 	1321 CCTCTGTAGAGAGGCCAGAGAGAATGGGTCATCCAGAAGATCCACGAGTCCCAGTTCAT 1380 	1381 CATTGTGGTTTGTTCCAAAGGTATGAAGTACTTTGTGGACAAGAAGAACTACAAACACAA 1440 	1441 AGGAGGTGGCCGAGGCTCGGGGAAAGGAGCTCTTCCTGGTGGCGGTGTCAGCCATTGC 1500	1501 CGAAAAGCTCCGCCAGGCCAAGAAGTTCGTCCGCGGCGCTCAGCAAGTTTATCGCCGT 1560 	1 CTACTTTGATTATTCCTGCGAGGGAGGCGCCCGGTATCCTAGACCTGAGTACCAAGTA 1	1523 CTACTTTGATTATTCCTGCGAGGGAGACGTCCCCGGTATCCTAGACCTGAGTACCAAGTA 1582 1621 CAGACTCATGGACAATCTTCCTCAGCTCTTCCCACTTGCACTCCCGAGACCACGGCCT 1680

	Qy 147 CGCAGCTGGCTGGCCGCTGGCGGCCCGCGCGCGCGCGCCCACACCTGTGGCT 206 L	QY 207 GGAGGATGAAAGCGGCTGCCCGACCCCGGCTTTGTGTTGCTAATGAGGGAGTGGGGCCCAG 266	Qy 267 CCAGCAGAACAGGACTGTACAACATCACCTTCAAATATGACAATTGTACCACCTACT 326	Qy 32.7 TGAATCCAGTGGGGAAGCATGTGATTGCTGACGCCCAGAATATCACCATCAGCCAGTATG 386	Qy 387 CTTGCCATGACCAAGTGGCAGTCACCATCTTTTGGTCCCCAGGGGCCCTCGGCATCGAAT 446 Db 329 CTTGCCATGACTAGTGCCAGTCACCATTCTTTGGTCCCCAGGGCCCTCGGCATCGAAT 388	Qy	Oy 507 AACTGATTCTAAAGGATCCGAAGCAGCTCAACAGTAGCTTCAAAAGAACTGGAATGGAAT 566	Qy 567 CTCAACCTTTCCTGAATATGAAACTTTGAAAAGGGATTATTTCGTAAAGGTTGTCCCTTTTT 626	Qy 627 CTTCCATTAAAAACGAAAGCAATTACCACCCTTTCTTCTTTAGAACCGGAGCCTGTGACC 686	QY 687 TGTTGTTACAGCCGGACAATCTAGCTTGTAAACCCTTCTGGAAGCCTCGGAACCTGAACA 746 Db 626 TGTTGTTACAGCCGGACAATCTAGCTTGTAAACCCTTCTGGAAGCCTCGGAACCTGAACA 685	QY 747 TCAGCCAGGAGAGACATGCAGGGGTGTCCTTCGACCATGCACGACAACTTCGGCT 806 Db 686 TCAGCCAGCATGGCTCGACATGCAGGTGTCCTTCGACCACGCACG	Oy 1CCGTTTCTATCTTCACTACAAGCTCAAGCACGAAGGACCTTTCAAGCGGAAAGACCT 866	Qy 867 GTAAGCAAACTACAGAGACGAACGACGACCAGCTGCCTCCTCAAAATGTTTCTCCAGGGG 926 Db 806 GTAAGCAGGAGCAAACTACAGAGATGACCAGCTGCCTCCTTCAAAATGTTTCTCCAGGGG 865	Oy 927 ATTATATAATTGAGCTGGTGGATGACACAACAACAAGAAAAGTGATGCATTATGCCT 986	987	OY 1047 TGGTAGTCATATCGCGACGCTCTTCACTGTGATGTGCGCACAGAAGAAG 1106	Qy 1107 AAAATATATATATCACATTTAGATGAGAGCCTCTGAGTCTTCCACATACACTGCAGCAC 1100	1167 TOTO BARBARA TOTO BARBARA TOTO BARBARA TOTO TOTO TATA TOTO TATA TOTO TABLET TO TOTO TABLET TO TABLET TO T
2123 GATGGAAGGACTCTCGACGACCAGACAGAAACGTCTTCCCTGACGAGAGCGTGTCCCC 2182	2221 CTCTTCAGGCCTGGGTGAGGAACCTCCTGCCCTTCCAAGCTCCTCTTCTGG 2280 	2281 GTCATGCAAAGCAGATCTTGGTTGCCGCAGCTACACTGATGAACTCCACGGGGTCGCCCC 2340 2243 GTCATGCAAAGCAGATCTTGGTTGCCGCAGCTACACTGATGAACTCCACGCGGTCGCCCC 2302	2341 TITGIAACAAAAGGAAAGAGTCIAAGCAITGCCACTITAGCTG 2383 	ULT 9 09-863-818A-9		TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS FILE REFERENCE: DX01170K CURRENT APPLICATION NUMBER: US/09/863,818A CURRENT FILING DATE: 2001-05-23	PRIOR APPLICATION NUMBER: US 60/206,862 PRIOR FILING DATE: 2000-05-24 SOFTWARE: PSEQ ID NOS: 22 SOFTWARE: Patentin version 3.1	SEQ ID NO 9 LENGTH: 2786 TYPE: DNA ORGANISM: Homo sapiens	FEATURE: NAME/KEY: CDS LOCATION: (70)(2283) OTHER INFORMATION:	NAME/KEY: mat_peptide LOCATION: (118)() OTHER INFORMATION: NAME/KEY: misc_feature	LOCATION: (8)(8) OTHER INFORMATION: unknown amino NAME/KEY: misc feature LOCATION: (1447(144)	OTHER INFORMATION: unknown amino NAME/KEY: misec feature LOCATION: (170)(170) amino OTHER INFORMATION: unknown amino	NAME/KEY: misc_feature LOCATION: (1947). (1194) OTHER INFORMATION: unknown amino NAME/KEY: misc_feature	LOCATION: (442)(442) OTHER INFORMATION: unknown amino NAME/KEY: misc feature	OTHER INFORMATION: unknown amino NAME/KEY: misc feature LOCATION: (519)(519). OTHER INFORMATION: unknown amino	ore 2218.6; DB 10; Length 2786; ed. No. 0;	Vallve U; Mismalcnes ZU; Indels 45; Caps GGGGGGGGGGGGGGGGAGGGCAGGGCTGGCTGGCGGAGGGCAGGCCA	11 CGGGCCÁGCAGCGGGGCGCGGGGCGCAGAGAACGGCCTGGCTGGCGGGGGGCGCACGGCCA 70

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US-10-749-144-9
US-10-749-144-9
Sequence 9, Application US/10749144
Publication No. US20040197306A1
GENERAL INFORMATION: Daniel M.
TITLE OF INVENTION: MARMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
FILE REFERENCE: DX01170K1
CURRENT APPLICATION NUMBER: US/10/749,144
CURRENT APPLICATION NUMBER: US 60/206,862
PRIOR PRILOR PILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.2
SEQ ID NO 9
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LOCATION: (519)..(519)
OTHER INFORMATION: unknown amino
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NAME/KEX: misc_feature
LOCATION: (475)..(475)
OTHER INFORMATION: unknown amino
                                                                                                                                               2306 CATTGCCACTTTAGCTG 2322
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LOCATION: (118)..()
FEATURE:
NAME/KEY: misc_feature
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OTHER INFORMATION: unknown an
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LOCATION: (8). (8)
OTHER INFORMATION: unknown
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LOCATION: (170)..(170)
OTHER INFORMATION: unknown
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LOCATION: (194)...(194)
OTHER INFORMATION: unknown
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NAME/KEY: misc feature
LOCATION: (442)...(442)
OTHER INFORMATION: unknown
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ORGANISM: Homo sapiens
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NAME/KEY: (
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Qy 2307 GCAGCTACACTGATGAACTCCACGCGGTCGCCCCTTTGTAACAAAACGAAAGAGTCTAAG 236 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	27	
2367 CATTGCCACTTTAGCTG 2383	Oy 87 TGGCCC Db 71 TGGCCC	CCGTGGCTGCAGCTCTGCTCCTTCTTTACGGTCAACGCCTGCCT
Db 2306 CATTGCCACTTTAGCTG 2322 RESULT 11	Oy 147 CGCAGC	GCAGCTGGCTGTGGCGGGTCCGGCCGCGCGGGGGGCGCCGACACCTGTGGCT 206
US-10-924-667-9 ; Sequence 9, Application US/10924667 ; Publication No. US20050009145A1 ; GENERAL INFORMATION:	207	GGAGGATGAAAGCGGCTGCCCGACCCCGGCTTTGTGTTGCTAATGAGGGGGTGGGGCCAG 266
APPLICANT: Gorman, Daniel M. TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND TITLE OF INVENTION: METHODS FILE REPERENCE: DX01.170K	267 C 209 C	CAGCAGAAACAGTGGGCTGTACAACATCACCTTCAAATATGACAATTGTACCACCTACT 326
CURRENT APPLICATION NUMBER: US/10/924,667 CURRENT FILING DATE: 2004-08-23 PRIOR APPLICATION NUMBER: US/09/863,818 PRIOR FILING DATE: 2001-05-23	Oy 327 TGAATC Db 269 TGAATC	GAATCCAGTGGGGAAGCATGTGATTGCTGACGCCCAGAATATCACCATCAGCCAGTATG 386
 PRIOR APPLICATION NUMBER: US 60/206,862 PRIOR FILING DATE: 2000-05-24 NUMBER OF SEQ ID NOS: 22 SOFTWARE: Patentin version 3.1 	Oy 387 CTTGCC 	CTTGCCATGACCAAGTGGCAGTCACCATTCTTTGGTCCCCAGGGGCCCTCGGCATCGAAT 446
; SEQ ID NO 9 ; LENGTH: 2786 ; TYPE: DNA ; ORGANISM: Homo sapiens	Qy 447 TCCTGA Db 389 TCCTGA	CCTGAAAGGATTTCGGGTAATACTGGAGGGCTGAAGTCGGAGGGAAGACAGTGCCAAC 506
FRATURE: NAMMYKEY: CDS LOCATION: (70)(2283) OTHER INFORMATION:	Oy 507 AACTGA Db 449 AACTGA	aactgattctaaaggatccgaagcagctcaacagtagcttcaaaagaactggaatggaat
FRATURE: NAME/KEY: mat_peptide LOCATION: (118) () COTHER INFORMATION:	Oy 567 CTCAAC Db 509 CTCAAC	CTGAACCTTTCCTGAATATGAAATTTGAAACGGATTATTTCGTAAAGGTTGTCCCTTTTC 626
FEATURE: FAME/KEY: misc_feature LOCATION: (8)(8) OTHER_INFORMATION: unknown amino	Oy 627 CTTCCA Db 566 CCTTCA	CTTCCATTAAAACGAAAGCAATTACCACCCTTTCTTTTAGAACCCGAGCCTGTGACC 686
FEATURE: NAME/KEY: misc_feature LOCATION: (144) COTHER_INFORMATION: unknown amino	Oy 687 TGTTGT Db 626 TGTTGT	TGTTGTTACAGCCGGACAATCTAGCTTGTAAACCCTTCTGGAAGCCTCGGAACCTCGAACA 746
FEATURE: NAME/KEY: misc_feature LOCATION: (170)(170) OTHER INFORMATION: unknown amino	Oy 747 TCAGCCAGC Db 686 TCAGCCAGG	AGCATGGCTCGGACATGCAGGTGTCCTTCGACCATGCACGCGCACAACTTCGGCT 806
FEATURE: NAME/KEY: misc_feature I.OCATION: (194) OTHER INFORMATION: unknown amino OTHER INFORMATION: unknown amino	Qy 807 TCGTT Db 746 TCGTT	ICCGTTTCTTCTATCTTCACTACAAGCTCAAGCACGAAGGACCTTTCAAGCGAAAGACCT 866
FEATURE: NAME/KEY: misc feature LOCATION: (442)(442) OTHER INFORMATION: unknown amino	Qy 867 GTAAGC Db 806 GTAAGC	GTAAGCAGGAGCAAACTACAGAGACCAGCTGCCTCCTTCAAAATGTTTCTCCAGGGG 926
FEATURE: NAME/KEY: misc feature LOCATION: (475)(475) OTHER INFORMATION: unknown amino	Oy 927 ATTATATATTC	Taattgagctggtggatgacactaacacaacaagaaagtgatgcattatgcct 986
FATURE: NAME/KEY: misc feature LOCATION: (519)(519) OTHER INFORMATION: unknown amino	OY 987 TAAAGC Db 926 TAAAGC	NAAGCCAGTGCACTCCCCGTGGGCCGGGCCCATCAGAGCCGTGGCCATCACAGTGCCAC 1046
US-10-924-667-9 Query Match 93.1%; Score 2218.6; DB 21; Length 2786;	Oy 1047 TGGTAG 100 986 TGGTAG	GGTAGTCATATCGGCATTCGCGACGCTCTTCACTGTGATGTGCCGCAAGAAGCAACAAG 1106
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Best Local Similarity 97.9%;
Matches 2271; Conservative C
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US-09-809-567-1
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                                                                                                                                      GGGTCATCCAGAAGATCCACGAGTCCCAGTTCATCATTGTGGGTTTGTTCCAAAGGTATGA 1406
                                                                                                                                                                                AGTACTTTGTGGACAAGAAGAACTACAAACACAAAGAGGTGGCCGAGGCTCGGGGAAAG 1466
                                                                                                                                                                                                                           GAGAGCTCTTCCTGGTGGCGGTGTCAGCCATTGCCGAAAAAGCTCCGCCAGGCCAAGCAGA 1526
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		olecules and Uses Thereof	CURRENT FILING DATE: 2003-07-10 PRIOR APPLICATION NUMBER: 09/809,567 PRIOR PILING DATE: 2001-03-15 PRIOR APPLICATION NUMBER: 09/724,460 PRIOR FILING DATE: 2000-11-28 PRIOR PILING DATE: 2000-03-16 PRIOR APPLICATION NUMBER: 60/189,816 PRIOR FILING DATE: 2000-03-16 DINMBER OF SEC 1D NOS: 19	5.0	US-10-616-788-1 Query Match Query Match Best Local Similarity 97.9%; Score 2215.4; DB 18; Length 3083; Best Local Similarity 97.9%; Pred. No. 0; Matches 2271; Conservative 0; Mismatches 6; Indels 42; Gaps 1; Q Qy 65 TGGCTGGGCGAGGCCACGGCCCTGGCTCTCTCTTACG 124 D Qy 65 IGGCTGGGCGAGGCCACGGCCCCTGGCTCTCTCTTACG 124 D	GCGCG 184 GCGCG 120 GCGCG 120 GTGTT 244 146 H

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; TITLE OF INVENTION: Therefor
FILE REFERENCE: MPI03-071PIRM
CURRENT APPLICATION NUMBER: US/10/842,006
CURRENT FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: 60/469522
PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 3
; LENGTH: 3083
                                                                                                                                                                                 Query Match 93.0%;
Best Local Similarity 97.9%;
Matches 2271; Conservative 0
                                                                                                                                          ; NAME/KEY: CDS
; LOCATION: (22)...(2241)
US-10-842-006-3
                                                                                                           TYPE: DNA ORGANISM: Homo Sapiens FEATURE:
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Sequence 3, Application US/10842006
Publication No. US20040235104A1
GENERAL INFORMATION:
APPLICANT: Yang, Runey-Bing
IITLE OF INVENTION: A Novel Human SEF Molecule and Uses

RESULT 15 US-10-842-006-3

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	GTGGTTTGTTCCAAAGGTATGAAGTACTTTGTGGACAAAGAAACTACAAAACAAAAGAA 133 GTGGTTTGTTCCAAAGGAAAGAAGACTCTTCCTGGTGGCGGTGTCACCAATGCCGAA 130 GGTGGCCGAAGGCTCGGGGAAGAGCTCTTCCTGGTGGCGGTTTATCGCCGTTGCCGAA 139 GGTGGCCGAGGCTCGGGGAAGAGCTCTTCCTGGTGGCGGTTTATCGCCGTTGCTGAA 139 AAGCTCCGCCAGGCCAAGCAGAGAGCTCTTCCTGGCGGTTTATCGCCGTCTAC 145 AAGCTCCGCCAGGCCAAGCAGAGAGTTCGTCCGGGGGGTGTTATTCGCCGTCTAC 145 AAGCTCCGCCAGGCAAGCAGAGAGACTCCTCGGGGGGTATCCTAGAACTTATCGCCGTCTAC 145 TTTGATTATTCCTGCAGAGAGACGTCCCGGGTATCCTAGACCTCAGATACAGTACAGTACAGA 161 TTTGATTATTCCTGCAGAGAGACGTCCCGGGTATCCTAGACCTCAGATACAGTACAGA 161 TTTGATTATTCCTGCAGAGAGACGTCCCGGGTATCCTAGACCTCAGAGTACAGATACAGA 161 TTTGATTATTCCTGCAGAGAGACGTCCCCGGGTATCCTAGACCTCAGGTACCAGGTACCAGGTACCTCAGGTACCTAGGACACACAGCAGAGACACCCCACTTGCTACAGACCTCCCGAGACCACAGGCACACAGGACACACAC	
	339 GGTGGCCGAGGCTCGGGGAGCTCTTCCTGGTGGCGGTGTCAGCCATTGCCGAA 1391 505 AAGCTCCGCCAGGCCAAGCAGAGTTCGTCGCGGGGCGTCAGCCATTGCCGAA 1391 399 AAGCTCCGCCAGGCCAAGCAGAGTTCGTCGCGGGCGCTCAGCAAGTTTATCGCCGTCTAC 156. 565 TTTGATTATTCCTGCGAGGGAGACGTCCCCGGTATCCTAGACCTGAGTACCAAGTACAGA 162. 611	
Search completed: Job time : 2871.87.	s TGTAGAGAGGCAGAGAATGGGTCATCCAGAAGATCCACGAGTCCCAGTTCATCATT 1	
217 217 234 223	1205 CTCTGCTATTCCAGTAAGATGGCCAGAATCACATGAATGTCGTCCAGTGTTTCGCCTAC 1264 1099 CTCTGCTATTCCAGTAAAGATGGCCAGAATCACATGAATGTCGTCCAGTGTTTCGCCTAC 1158 1265 TTCCTCCAGGACTTCTGGGCTGTGAGGTGGCTTGGGAAGACTTCAGCCTC 1124 1159 TTCCTCCAGGACTTCTGGGCTGTGAGGTGGCTCTGGAACAACTTCAGCCTC 1124 1159 TTCCTCCAGGACTTCTGTGGCTGTGAGGTGGCTCTGGGAACAACTTCAGCCTC 11218	
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DADAGCAGATCTTGGTTGCCGCAGCTACACTGATGAACTCCACGCGGTCGCCCCTTTG 2344 1938 GCCGCCCTGCAACCCCTGCACACGGTGAAAGCCGGCAGCCCCTCGGACATGCCG 2104 GACTCAGGCATCTATGACTCGTCTGTGCCCTCATCCGAGCTGTCTCTGCCACTGATG 2164 4GCCTGGGTGAGGAACCTCCTGCCCTTCCTTCCAAGCTCCTCTTCTGGGTCA 2284 AGACTCTCGACGGACCACACAGAACGTCTTCCCTGACGGAGAGCGTGTCCTCT 2224 2044 ACAAAACGAAAGACTAAGCATTGCCACTTTAGCTG 2383

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8 US-10-717-282-13

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9 US-10-767-701-12124

6 US-10-329-079-34

6 US-10-329-079-34

7 US-10-283-94316

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0.05-10-608-449-1

0.05-099-567-1

1.05-10-216-156-1

3.05-10-216-156-1

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0.05-09-863-818A-9

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; Sequence 1, Application US/09912157
; Patent No. US20020165348A1
; GENERAL INFORMATION:
    APPLICANT: Freshell, Scott R.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Human Cytokine Receptor
; TITLE REFERENCE: 00-49
; CURRENT APPLICATION NUMBER: US/09/912,157
; CURRENT FILING DATE: 2001-07-23
; SUFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO:
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ORGANISM: Homo sapiens
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(cgn2_6/ptodata1/fpubpna/USO7_PUBCOWB.seq:*

(cgn2_6/ptodata1/fpubpna/USO6_PUBCOWB.seq:*

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(cgn2_6/ptodata1/fpubpna/USO6_PUBCOMB.seq:*

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Listing first 45 summaries
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LENGTH: 2383
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US-09-912-157-7
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US-10-717-282-4
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100.0%; Score 149; DB 9;
Best Local Similarity 100.0%; Pred. No. 4.3e-35;
Matches 149; Conservative 0; Mismatches 0;
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Sequence 1, Application US/10717282
Sequence 1, Application US/10717282
Publication No. US20040077052A1
GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: Ruestner, Rolf E.
APPLICANT: Gao, Zeren
TITLE OF INVENTION: Human Cytokine Receptor
FILE REFERENCE: 00-49
CURRENT APPLICATION NUMBER: US/10/717,282
CURRENT PILING DATE: 2003-11-19
PRIOR RILING DATE: 2001-07-24
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTHAL 2383
                                                                                                                                                                                               Sequence 4, Application US/09912157
; Sequence 4, Application US/09912157
; Patent No. US20020165348A1
; GENERAL INFORMATION:
   APPLICANT: Presenell, Scott R.
   APPLICANT: Gao, Zeren
   TITLE OF INVENTION: Human Cytokine Receptor
   TITLE OF INVENTION: Human Cytokine Receptor
   CURRENT APPLICATION NUMBER: US/09/912,157
   CURRENT FILING DATE: 2001-07-23
   NUMBER OF SEQ ID NOS: 13
   SOFTWARE: FastSEQ for Windows Version 3.0
   SEQ ID NO 4
   LENGTH 2383
                                                                                                     206 TGGAGGATGAAAGCGGCTGCCCGACCCCG 234
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NAME/KEY: CDS
LOCATION: (86)...(2344)
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; LOCATION: (86)...(2344)
US-09-912-157-4
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ORGANISM: Homo sapiens
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100.0%; Score 149; DB 18; Length 2383; 100.0%; Pred. No. 4.3e-35; ive 0; Mismatches 0; Indels 0;
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Patent No. US20020165348A1
GENERAL INFORMATION:
APPLICANT: Freshell, Scott R.
APPLICANT: Gao, Zeren
TITLE OF INVENTION: Human Cytokine Receptor
FILE REFERENCE: 00-49
CURRENT APPLICATION NUMBER: US/09/912,157
CURRENT FILING DATE: 2001-07-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Presnell, Scott R.
APPLICANT: Kuestner, Rolf E.
APPLICANT: Goo, Zeren
TITLE OF INVENTION: Human Cytokine Receptor
FILE REFERENCE: 00-49
CURRENT APPLICATION NUMBER: US/10/717,282
CURRENT FILING DATE: 2003-11-19
PRIOR APPLICATION NUMBER: US/09/912,157
PRIOR APPLICATION NUMBER: US/09/912,157
RIGHER OF END DATE: 2001-07-24
NUMBER OF END ID NOS: 13
SOFTWARE: FASTSEQ for Windows Version 3.0
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Best Local Similarity 100.
Matches 149; Conservative
                                                  Matches 149; Conservative
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; LOCATION: (86)...(2344)
US-10-717-282-4
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ORGANISM: Homo sapiens
  Query Match
Best Local Similarity
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Publication No. US20040038242A1
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LENGTH: 4392
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US-10-842-006-1
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                                                                                                                                                                                                  85.2%; Score 127; DB 9; Length 2341; 93.0%; Pred. No. 1.6e-28; tive 0; Mismatches 10; Indels (
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| Sequence 7, Application US/10717282
| Publication No. US20040077052A1
| GENERAL INFORMATION:
| APPLICANT: Freenell, Scott R.
| APPLICANT: Kuestner, Rolf E.
| APPLICANT: Goo, Zeren
| TILLE OF INVENTION: Human Cytokine Receptor
| TILLE OF INVENTION: Human Cytokine Receptor
| TILLE OF INVENTION: Human Cytokine Receptor
| TILLE OF INVENTION: Human Cytokine Receptor
| TILLE OF INVENTION: Human Cytokine Receptor
| TILLE OF INVENTION: Human Cytokine Receptor
| TILLE OF INVENTION NUMBER: US/10/717,282
| CURRENT FILING DATE: 2001-07-24
| NUMBER OF SEQ ID NOS: 13
| SOFTWARE: FastSEQ for Windows Version 3.0
 NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
LENGTH: 2341
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Best Local Similarity 93.03
Matches 133; Conservative
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; LOCATION: (86)...(2302)
US-10-717-282-7
                                                                                                                            ; NAME/KEY: CDS
; LOCATION: (86)...(2302)
US-09-912-157-7
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ORGANISM: Homo sapiens
                                                                         TYPE: DNA
ORGANISM: Homo sapiens
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LENGTH: 2341
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US-10-717-282-7
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US-10-343-348-15 ; Sequence 15, Application US/10343348

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GENERAL INFORMATION:
APPLICANT: Edmonds, Brian
APPLICANT: Micanovic, Radmila
APPLICANT: Micanovic, Radmila
APPLICANT: Ou, Weijia
APPLICANT: Su, Eric
APPLICANT: Techang, Sheng-Hung
APPLICANT: Wang, He
TITLE OF INVENTION: No. US20040038242Alel secreted proteins and their uses
FILE REFERENCE: X-14001
CURRENT PFLICATION NUMBER: US/10/343,348
CURRENT FILING DATE: 2003-01-29
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.1
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TITLE OF INVENTION: A Novel Human SEF Molecule and Uses
TITLE OF INVENTION: Therefor
TITLE OF INVENTION: Therefor
FILE REFERENCE: MRI03-071PIRM
CURRENT FILING DATE: 2004-05-07
PRIOR PILING DATE: 2003-05-08
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FSELEGO for Windows Version 4.0
SEQ ID NO 1
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85.2%; Score 127; DB 20;
Best Local Similarity 93.0%; Pred. No. 1.5e-28;
Matches 133; Conservative 0; Mismatches 10;
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Best Local Similarity 93.0°
Matches 133; Conservative
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; LOCATION: (90)...(2309)
US-10-842-006-1
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ORGANISM: Homo Sapiens
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: mat_peptide
LOCATION: (82)..()
OTHER INFORMATION:
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LOCATION: (1)..(1662)
OTHER INFORMATION:
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; NAME/KEY: CDS
; LOCATION: (22)
US-10-216-156-1
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US-10-616-788-1
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Patent No. US20020045213A1;
GENERAL INFORMATION:
JAPLICANT: Jing, Shuqian
TITLE OF INVENTION:
CURRENT APPLICATION UNDER: US/09/809,567;
CURRENT FILING DATE: 2001-03-15;
PRIOR FILING DATE: 2000-11-28;
PRIOR PALICATION NUMBER: 09/724,460;
PRIOR APPLICATION NUMBER: 60/189,816;
PRIOR APPLICATION NUMBER: 60/189,816;
PRIOR APPLICATION NUMBER: 60/189,816;
PRIOR APPLICATION NUMBER: 60/189,816;
PRIOR PELING DATE: 2000-03-16;
SOFTWARE: PATENTING DATE: 2000-
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Publication No. US20040265834A1
GENERAL INNORMATION:
APPLICANT: Tainghua University
TITLE OF INVENTION: Human Interleukin-17 Receptor Like Molecule
FILE REFERENCE: 12003269C-US
CURRENT APPLICATION NUMBER: US/10/608,449
CURRENT FILING DATE: 2003-06-30
NUMBER OF SEQ ID NOS: 19
SOFTWARRE: Patentin version 3.1
SEQ ID NO 1
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Pred. No. 1.5e-28;
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Best Local Similarity 93.0%;
Matches 133; Conservative (
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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; LOCATION: (22)..(2235)
US-09-809-567-1
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TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof
TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof
FILE REFERENCE: 010.17/36916A
CURRENT APPLICATION NUMBER: US/10/216,156
CURRENT FILING DATE: 2002-08-08
PRIOR PELICATION NUMBER: US/9/809,567
PRIOR PELING DATE: 2001-03-16
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-03-16
NUMBER OF SEQ ID NOS: 17
SOSTWARE: Patentin Ver. 2.0
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Publication No. US20040048338A1
GENERAL INFORMATION:
APPLICANT: Jing, Shuqian
TITLE OF INVERTION: IL-17 Receptor Like Molecules and Uses Thereof
FILE REFERENCE: 01017/33525
CURRENT APPLICATION NUMBER: US/10/616,788
CURRENT PELING DATE: 2003-07-10
PRIOR PILING DATE: 2001-03-15
PRIOR FILING DATE: 2001-03-15
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Pred. No. 1.4e-27;
0; Mismatches 12; Indels 0;
  Length 3083;
                                         Indels
  DB 9;
Score 123.8; DB 9;
Pred. No. 1.4e-27;
0; Mismatches 12;
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Query Match
Best Local Similarity 91.6%;
Matches 131; Conservative
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Matches 131; Conservative
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ORGANISM: Homo sapiens
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US-09-863-818A-9
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US-10-749-144-9
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                                                                                                                                                                                                                                               DB 18; Length 3083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/10842006
| Fublication No. US20040235104A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Yang, Ruey-Bing
| TITLE OF INVENTION: A Novel Human SEF Molecule and Uses
| TITLE OF INVENTION: Therefor
| TITLE OF INVENTION: Therefor
| TITLE OF INVENTION: Therefor
| TITLE OF INVENTION: A NOVEL HUMAN CURRENT APPLICATION NUMBER: US/10/842,006
| CURRENT FILING DATE: 2004-05-07
| PRIOR PILING DATE: 2003-05-08
| NUMBER OF SEQ ID NOS: 12
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Pred. No. 1.4e-27;
0; Mismatches 12;
                                                                                                                                                                                                                                               Score 123.8; DB 1
Pred. No. 1.4e-27;
                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 3 LENGTH: 3083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 TGGAGGATGAAAGCGGCTGCCCG 143
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PRIOR APPLICATION NUMBER: 09/724,460 PRIOR FILING DATE: 2000-11-28 PRIOR APPLICATION NUMBER: 60/189,816 PRIOR FILING DATE: 2000-03-16 NUMBER OF SEQ ID NOS: 19 SOFTWARE: PATENTIN Ver. 2.0 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 83.1%;
Best Local Similarity 91.6%;
Matches 131; Conservative
                                                                                                                                                                                                                                              Query Match 83.1%;
Best Local Similarity 91.6%;
Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: CDS
; LOCATION: (22)...(2241)
US-10-842-006-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo Sapiens
                                                                                                                 LENGTH: 3083
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                            ; NAME/KEY: CDS
; LOCATION: (22)..(2235)
US-10-616-788-1
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US-10-842-006-3
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Sequence 9, Application US/09863818A

Publication No. US20030092881A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
CURRENT APPLICATION
CURRENT PILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US/09/863,818A

CURRENT FILING DATE: 2000-05-24

PRIOR APPLICATION NUMBER: US 60/206,862

PRIOR APPLICATION NUMBER: US 60/206,862

PRIOR APPLICATION NUMBER: US 60/206,862

NUMBER OF SEQ ID NOS: 22

NUMBER PEGE 1200-05-24

NUMBER PEGE 1200-05-24
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TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
FILE REPERENCE: DX01170K1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 TGGAGGATGAAAGCGGCTGCCCG 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (194)..(194)
OTHER INFORMATION: unknown amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (170)..(170)
OTHER INFORMATION: unknown amino
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OTHER INFORMATION: unknown amino
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LOCATION: (519)..(519)
OTHER INFORMATION: unknown amino
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LOCATION: (8)..(8)
OTHER INFORMATION: unknown
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LOCATION: (144)..(144)
OTHER INFORMATION: unknown
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OTHER INFORMATION: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: (70)..(2283)
OTHER INFORMATION:
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LOCATION: (442)..(442)
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LOCATION: (475)..(475)
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: mat_peptide
LOCATION: (118)..()
OTHER INFORMATION:
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(without alignments)
2696.128 Million cell updates/sec
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4013
1 MAPWLQLCSVFFTVNACLNG.......CKADLGCRSYTDELHAVAPL 753
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(cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
(cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
(cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
(cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
(cgn2_6/ptodata/2/pubpaa/Decuta/BubCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                               Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 2, Appli	Sequence 2, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 8, Appli	Seguence 8, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 2, Appli
	ID	US-09-912-157-2	US-10-717-282-2	US-09-912-157-5	US-10-717-282-5	US-09-912-157-8	US-10-717-282-8	US-10-842-006-2	US-10-608-449-2	US-10-842-006-4	US-09-809-567-2	US-10-216-156-2
	DB	6	15	σ	15	σ	15	16	16	16	σ	14
	Query Match Length DB	753	753	753	753	739	739	739	739	739	738	738
مد	Query Match	100.0	100.0	99.8	8.66	97.8	97.8	97.6	97.6	97.3	97.2	97.2
	Score	4013	4013	4003	4003	3925	3925	3915	3915	3905	3901	3901
	Result No.	п	7	e	4	Ŋ	9	7	80	6	10	11

Sequence 2, Appli Sequence 10, Appl Sequence 10, Appl Sequence 11, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl	Sequence 3, Appliance Sequence 3, Appliance 10, Appliance 107, Appliance 107, Appliance 107, Appliance 10, Appliance 10, Appliance 1, Appliance 1, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 19, Appliance 2, Appliance 19, Appliance 2, Appliance 19, Appliance 2, Appliance 19, Ap
US-10-616-788-2 US-10-749-1144-10 US-10-924-667-10 US-10-924-667-10 US-10-928-874-503-18 US-09-814-503-18 US-09-816-741-18 US-09-908-827-18 US-09-10-77-18 US-10-410-927-18 US-10-410-938-19 US-10-608-449-4 US-10-608-449-4 US-10-34-348-16 US-10-608-449-4 US-	US-10-216-158-3 US-09-778-971-9 US-10-033-522-1 US-10-207-655-107 US-10-742-161-10 US-10-742-372-10 US-10-646-308-4 US-10-918-084-1 US-10-742-161-2 US-10-742-161-2 US-10-742-372-2 US-10-742-372-2
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ALIGNMENTS

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61 ASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVTILWSPGALGIE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLKGFRVILEELKSEGROCQQLILKDPRQLNSSFKRTGMESQPFLNMKFETDYFVKVVPF 180
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                                                                                                                                                                                                                                                                                                                                                            Length 753;
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                                                                                                                                                                                                                                                                                                                                                              DB 9;
                                                                 APPLICANT: Presnell, Scott R.
APPLICANT: Evestner, Rolf E.
APPLICANT: Goo, Zeren
TITLE OF INVENTION: Human Cytokine Receptor
FILE REFERENCE: 00-49
CURRENT FILING DATE: 2001-07-23
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 753
                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 4013;
100.0%; Pred. No. 0;
ative 0; Mismatches
         Sequence 2, Application US/09912157; Patent No. US20020165348A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 753; Conservative
                                                                                                                                                                                                                                                                                       TYPE: PRT
CORGANISM: Homo sapiens
US-09-912-157-2
US-09-912-157-2
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TYPE: PRT
ORGANISM: Homo sapiens
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                      PSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKPRNLNISQHGSDMQVSFDHAPHNFG 240
FLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFKRTGMESQPFLNMKFETDYFVKVVPF 180
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APPLICANT: Kuestner, Rolf E.
APPLICANT: Gao. Zeren
ITLE OF INVENTION: Human Cytokine Receptor
FILE REFERENCE: 00-49
CURRENT APPLICATION NUMBER: US/10/717,282
CURRENT FILING DATE: 2003-11-19
PRIOR APPLICATION NUMBER: US/09/912,157
PRIOR FILING DATE: 2001-07-24
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 753; Conservative 0; Mismatches
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// Publication No. US20040077052A1
// GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-10-717-282-2
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Setent No. US20020165348A1
GENERAL INFORMATION:
APPLICANT: Fresnell, Scott R.
APPLICANT: Kuestner, Rolf E.
APPLICANT: Goo, Zeren
TILE OF INVENTION: Human Cytokine Receptor
FILE REFERENCE: 00-49
CURRENT APPLICATION UNMER: US/09/912,157
CURRENT FILING DATE: 2001-07-23
NUMBER OF SEQ ID NOS: 13
SOFTWARE FRAESEQ for Windows Version 3.0
SEQ ID NO S.
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Best Local Similarity 99.7%; Pred. No. 0;
Matches 751; Conservative 0; Mismatches
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            1 MAPWLQLCSVFFTVMACLNGSQLAVAAGGSGRARGADTCGWRWKAAARPRLCVANEGVGP
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Publication No. US20040077052A1

GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: Gao, Zeren
TITLE OF INVENTION: Human Cytokine Receptor
FILE REFRENCE: 00-49
FILE REFRENCE: 00-49
CURRENT APPLICATION NUMBER: US/10/717,282
CURRENT FILING DATE: 2003-11-19
PRIOR PAPPLICATION NUMBER: US/09/912,157
PRIOR FILING DATE: 2001-07-24
NUMBER OF SEQ ID NOS: 13
SOFWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
LEMOTH: 753
TYPE: PRT
COGGNISM: Homo sapiens
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US-10-717-282-5
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 Length
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   DB
; Score 4003; DB
; Pred. No. 0;
0; Mismatches
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APPLICANT: Kuestner, Rolf E.
APPLICANT: Gao, Zeren
TITLE OF INVENTION: Human Cytokine Receptor;
FILE REFERENCE: 00-49
CURRENT APPLICATION NUMBER: US/09/912,157
CURRENT FILING DATE: 2001-07-23
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/09912157; Patent No. US20020165348A1; GENERAL INFORMATION:
   99.8%;
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                                   Conservative
                  Similarity
   Query Match
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Matches 751;
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                                                       Score 3925; DE Pred. No. 0; 0; Mismatches
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Publication No. US20040077052A1
GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: Kuestner, Rolf E.
APPLICANT: Gao, Zeren
TITLE OF INVENTION: Human Cytokine Receptor
FILE REFERENCE: 00-49
                                                        97.8%;
98.1%;
                                                       Query Match
Best Local Similarity 98.1
Matches 739; Conservative
                  ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-912-157-8
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US-10-717-282-8
SEQ ID NO 8
LENGTH: 739
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; Pred. No. 0;
0; Mismatches
CURRENT APPLICATION NUMBER: US/10/717,282
CURRENT FILING DATE: 2003-11-19
PRIOR APPLICATION UNMERR: US/09/912,157
PRIOR FILING DATE: 2001-07-24
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO
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US-10-842-006-2
Sequence 2, Application US/10842006
; Publication No. US20040235104A1
                                                                                                                                                                                    Query Match 97.8%;
Best Local Similarity 98.1%;
Matches 739; Conservative (
                                                                                                                         TYPE: PRT
CORGANISM: Homo sapiens
US-10-717-282-8
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PPALPSKILSSGSCKADLGCRSYTDELHAVAPL 753
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Best Local Similarity 97.9%;
Matches 737; Conservative 1
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CRGANISM: Homo sapiens
US-10-608-449-2
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                                                                                                                                                             Length 739;
APPLICANT: Yang, Rhey-Bing;
TITLE OF INVENTION: A Novel Human SEF Molecule and Uses;
TITLE OF INVENTION: Therefor
FILE REPERENCE: MPIO3-071PIRM;
CURRENT APPLICATION NUMBER: US/10/842,006
CURRENT FILING DATE: 2004-05-07
PRIOR PILING DATE: 2003-05-08
NUMBER OF SEQ ID NOS: 12
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 2
LENGTH: 739
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                                                                                                                                                             97.6%;
                                                                                                                                                                                Conservative
                                                                                                                       TYPE: PRT
ORGANISM: Homo Sapiens
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Best Local Similarity
Matches 737; Conserv
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US-10-608-449-2
US-10-608-449-2
; Sequence 2, Application US/10608449
; Publication No. US20040265834A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Human Interleukin-17 Receptor Like Molecule
FILE REFERENCE: 12003269C-US
; CURRENT FILING DATE: 2003-06-30
NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 739 14; Length 739; Indels Score 3915; DB 16; Pred. No. 0; 1; Mismatches 1;

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                                                 Sequence 4, Application US/10842006

Publication No. US20040235104A1

GENERAL INFORMATION:

APPLICANT: Yang, Ruey-Bing

TITLE OF INVENTION: A Novel Human SEF Molecule and Uses

TITLE OF INVENTION: Therefor

FILE REFERENCE: MPT03-071P1RM

CURRENT APPLICATION NUMBER: 05/10/842,006

CURRENT FILING DATE: 2004-05-07

PRIOR PILING DATE: 2003-05-08

NUMBER OF SEQ ID NOS: 12

SOFTWARE: FRAESEQ for Windows Version 4.0

SEQ ID NO 4.0
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PPALPSKLLSSGSCKADLGCRSYTDELHAVAPL 739
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Best Local Similarity 97.6%; Pred. No. 0;
Matches 735; Conservative 1; Mismatches
                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo Sapiens
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US-10-842-006-4
                                            -10-842-006-4
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; Sequence 2, Application US/09809567
; Patent No. US20020045213A1
; GENERAL INFORMATION:
; APPLICANT: Jing, Shugh
; TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof
; FILE REFERENCE: 01017/36916A
; CURRENT PELING DATE: 2001-3-15
; PRIOR APPLICATION NUMBER: US/09/809,567
; PRIOR APPLICATION NUMBER: 09/724,460
; PRIOR APPLICATION NUMBER: 60/189,816
; PRIOR APPLICATION NUMBER: 60/189,816
; PRIOR APPLICATION NUMBER: 60/189,816
; PRIOR APPLICATION NUMBER: 60/189,816
; RUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 738
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Best Local Similarity 97.6%; Pred. No. 0;
Matches 734; Conservative 1; Mismatches
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US-09-809-567-2
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SSSAALSKFIAVYPDYSCECDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTR
                        467 SSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPQQHTR
                                                                                          QGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFEKQFVPFHPPPLRYREPVLEKFDSGL
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US-10-616-788-2
; Sequence 2, Application US/10616788
; Publication No. US20040048338A1
; Publication No. US20040048338A1
; GENERAL INFORMATION:
; APPLICANT: Jing, Shuqian
; TITLE OF INVENTION: L1-17 Receptor Like Molecules and Uses Thereof
; FILE REFERENCE: 01017/35525
; CURRENT APPLICATION NUMBER: US/10/616,788
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 09/809,567
; PRIOR FILING DATE: 2001-03-15
; PRIOR FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-11-68
; RIOR APPLICATION NUMBER: 60/189,816
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PATCHILING OF 2000-03-16
; SOFTWARE: PATCHILING DATE: 2000-03-16
; SOFTWARE: PATCHILING DATE: 2000-03-16
; SOFTWARE: PATCHILING DATE: 2000-03-16
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97.2%; Score 3901; Di
Best Local Similarity 97.6%; Pred. No. 0;
Matches 734; Conservative 1; Mismatches
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US-10-616-788-2
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                                                                                                                                                                                             ; Score 3901; DE; Pred. No. 0; 1; Mismatches
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Best Local Similarity 97.6%;
Matches 734; Conservative 1
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US-10-216-156-2
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NAME/KEY: misc_feature
; LOCATION: (194)...(194)
; OTHER INFORMATION: unknown amino;
; NAME/KEY: misc_feature
; LOCATION: (442)...(442)
; OTHER INFORMATION: unknown amino;
; NAME/KEY: misc_feature
; LOCATION: (475)...(475)
; OTHER INFORMATION: unknown amino;
; LOCATION: (519)...(519)
; COCATION: (519)...(519)
; OTHER INFORMATION: unknown amino;
; COCATION: (519)...(519)
; OTHER INFORMATION: unknown amino;
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US-10-749-144-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: GOTTON Daniel M.

TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS FILE REFERENCE: DX01170K
CURRENT APPLICATION NUMBER: US/09/863,818A
CURRENT PILING DATE: 2001-05-23
PRIOR PPLICATION NUMBER: US 60/206,862
PRIOR PILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
LENGTH: 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or Met
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LOCATION: (18)...(18)

OTHER INFORMATION: The 'Xaa' at location 18 stands for Gln, Arg, Pro, or Lecators in the 'Xaa' at location 26 stands for Lys, Arg, Thr, or Me (1207-10): The 'Xaa' at location 26 stands for Lys, Arg, Thr, or Me (1207-10): The 'Xaa' at location 109 stands for Lys, Arg, Thr, or Me (1207-10): The 'Xaa' at location 109 stands for Ser, Gly, Arg, or C (1207-10): The 'Xaa' at location 109 stands for Ile, Val, Leu, or C (1207-10): The 'Xaa' at location 120 stands for Ile, Val, Leu, or Phenemanner in the 'Xaa' at location 134 stands for Ile, Val, Leu, or Phenemanner in the 'Xaa' at location 134 stands for Leu, or Phenemanner in the 'Xaa' at location 134 stands for Leu, or Phenemanner in the 'Xaa' at location 134 stands for Leu, or Phenemanner in the 'Xaa' at location 134 stands for Leu, or Phenemanner in the 'Xaa' at location 134 stands for Leu, or Phenemanner in the 'Xaa' at location 134 stands for Leu, or Phenemanner in the 'Xaa' at location 134 stands for Leu, or Phenemanner in the 'Xaa' at location 134 stands for Leu, or Phenemanner in the 'Xaa' at location 134 stands for Leu, or Phenemanner in the 'Xaa' at location 134 stands for Leu, or Phenemanner in the 'Xaa' at location 134 stands for Leu, or Phenemanner in the 'Xaa' at location 134 stands for Leu, or Phenemanner in the 'Xaa' at location 134 stands for Leu, or Phenemanner in the 'Xaa' at location 134 stands for Leu, or Phenemanner in the 'Xaa' at location 134 stands for Leu, or Phenemanner in the 'Xaa' at location 134 stands for Leu, or Phenemanner in the 'Xaa' at location 134 stands for Leu, or Phenemanner in the 'Xaa' at location 134 stands for Leu, or Phenemanner in the 'Xaa' at location 134 stands for Leu, or Phenemanner in the 'Xaa' at location 134 stands for Leu, or Phenemanner in the 'Xaa' at location 134 stands for Leu, or Phenemanner in the 'Xaa' at location 134 stands for Leu, or Phenemanner in the 'Xaa' at location in the 'Xaa' at location in the 'Xaa' at location in the 'Xaa' at location in the 'Xaa' at 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAALQPL 660
                                                                                                                                                   WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQ 480
                                                                                                                                                                                 SSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTR 540
                                                                                                                                                                                                                                                                                                                                                                                                                     QGSRRNYFRSKSGRSLYVAICNWHQFIDEEPDWFEKQFVPFHPPPLRYKBPVLEKFDSGL 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              587 VIANDVMCKPGPESDFCLKVEAPVLGATGPADSQHESQHGGLDQDGEARPALDGSAALQPL 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LHTVKAGSPSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSGLGEEE 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LHTVKAGSPSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSSGLGEEE 706
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                                      LPRERLRPRPKVFLCYSSKDGONHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQRE
                                                                                                                                                                                                                                                                                                    SSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMDNLPOLCSHLHSRDHGLOEPGOHTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPALPSKLLSSGSCKADLGCRSYTDELHAVAP 738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 10, Application US/09863818A; Publication No. US20030092881A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (8). (8)
OTHER INFORMATION: unknown amino
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OTHER INFORMATION: unknown amino
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OTHER INFORMATION: unknown
NAME/KEY: misc feature
LOCATION: (170)...(170)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
US-09-863-818A-10
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Publication No. US200S0009145A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS
TITLE REFERENCE: DOI 1070

CURRENT APPLICATION NUMBER: US/10/924,667

CURRENT PILING DATE: 2004-08-23

PRIOR APPLICATION NUMBER: US/09/863,818

PRIOR APPLICATION NUMBER: US/09/862

PRIOR APPLICATION NUMBER: US 60/206,862

PRIOR FILING DATE: 2000-05-24

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PetentIn version 3.1

SEQ ID NO 10
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                                          466 SSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTR
                                                                                                                                                                                           601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAALQPL
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                                                                                               QGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFEKQFVPFHPPPLRYREPVLEKFDSGL
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LOCATION: (109)..(109).
OTHER INFORMATION: The 'Xàa' at location 109 stands for Ser, Gly, Arg,
OTHER INFORMATION: Cys.
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NAME/KEY: misc_feature
LOCATION: (26)..(26)
OTHER INFORMATION: The 'Xaa' at location 26 stands for LyB, Arg,
OTHER INFORMATION: Met.
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LOCATION: (18)...(18)
OTHER INFORMATION: The 'Xaa' at location 18 stands for Gln, Arg,
OTHER INFORMATION: Leu.
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OTHER INFORMATION: The 'Xaa' at location 120 stands
OTHER INFORMATION: Phe.
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                                                                                                                                                                                                                                                                                                                                                     100 PPALPSKLLSSGSCKADLGCRSYTDELHAVAPL 738
                                                                                                                                                                                                                                                                                                                          721 PPALPSKLLSSGSCKADLGCRSYTDELHAVAPL 753
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OTHER INFORMATION: unknown amino FEATURE:
NAME/KEY: misc_feature
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OTHER INFORMATION: The
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ORGANISM: Homo sapiens
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US-10-924-667-10
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Sequence 10, Application US/10749144

Publication No. US20040197306A1

GENERAL INFORMATION:

APPLICANT: Gorman, Daniel M.

TITLE OF INVENTION: MAWMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS TILE REPERCECE: DX01170K1

CURRENT APPLICATION NUMBER: US/10/749,144

CURRENT FILING DATE: 2003-12-29

PRIOR APPLICATION NUMBER: US 60/206,862

PRIOR PELING DATE: 2000-05-24

NUMBER OF SEQ ID NOS: 24

SEQ ID NO 10

LENGTH: 738
                                                                                                                                                                                                                                                                                                                                                                     Len.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FLKGFRVILEELKSEGROCOOLILKDPKOLNSSFKRTGMESQPFLNMKFETDYFVKVVPF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 FLKGFRVILEELKSEGRQXQQLILKDPKQXNSSFKRTGMESQPXLNMKFETDYFVR-LSF 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQQENIYSHLDEESSESSTYTAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQQENIYSHLDEESSESSTYTAA 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQRE 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQ 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASRNSGLYNITEKYDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVTILWSPGALGIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAPWLQLCSVFFTVNACLNGSQLAVAAGGSGRARGADTCGWRMKAAARPRLCVANEGVGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAPWLQLCSVPFTVNACLNGSQLAVAAGGSGRAXGADTCSW------XGVGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 PSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKPRNLNISQHGSDMQVSFDHAPHNFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arg,
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                                                                                                                                                                                                                                                                                                                                                                     Pro,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gly,
                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (18)..(18)
OTHER INFORMATION: The 'Xaa' at location 18 stands for Gln, Arg,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Arg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        at location 134 stands for Leu, or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ser,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             at location 120 stands for Ile,
                                                                                                                                                                                                                                                                                                                                                                                                                                             for Lys,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     at location 109 stands
                                                                                                                                                                                                                                                                                                                                                                                                                                           26 stands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 3835.5;
Pred. No. 0;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             at location
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 95.6%;
Best Local Similarity 96.4%;
Matches 726; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature

: LOCATION: (134)

: CTHER INFORMATION: The 'Xaa'

US-10-749-144-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Xaa'
                                                                                                                                                                                                                                                                                                                                                                                                                                               'Xaa'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Xaa'
                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (26)...(26)
OTHER INFORMATION: The
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LOCATION: (120)..(120)
OTHER INFORMATION: The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KBY: misc feature
LOCATION: (109)...(109)
OTHER INFORMATION: The
                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ASRNSGLYNITEKYDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVTILWSPGALGIE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 PSIKNESNYHPFFFRTRACDLLLQPDNIACKPFWKPKNINISQHGSDMQVSFDHAPHNFG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             166 SFIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKPRNLNISQHGSDMQVSFDHAPHNFG 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            286 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVWCRKKQQENIYSHLDEESSESSTYTAA 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQ 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    406 WVIQXIHESQPIIVVCSKGMKYFVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQ 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTR 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FLKGFRVILBELKSEGRQCQQLILKDPKQLNSSFKRTGMESQPFLNMKFETDYFVKVVPF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRFFYLHYKLKHEGPFKRKTCKQEQTTETTSCLLQNVSPGDYIIBLVDDTNTTRKVMHYA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQQENIYSHLDEESSESSTYTAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQRE 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VINDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGBARPALDGSAALQPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MAPWLQLCSVFFTVNACLNGSQLAVAAGGSGRARGADTCGWRMKAAARPRLCVANEGVGP
                                                                                                                                                                                                                                                                                                                                                                                       DB 17; Length 738;
                                                                                                                                                                                                                                                                                                                                                                                                                     15;
                                                                                                                                                                                                                                                                                                                                                                                                                      10; Indels
                                                                                                                                                                                                                                                                                                                                                                                     95.6%; Score 3835.5; 96.4%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
LOCATION: (144)...(144)

PEATURE:
NAME/KEX: misc feature
LOCATION: (170)

OTHER INFORMATION: unknown amino
FEATURE:
NAME/KEX: misc feature
LOCATION: (1947)...(194)

NAME/KEX: misc feature
LOCATION: (1947)...(194)

OTHER INFORMATION: unknown amino
FEATURE:
FEATURE:
NAME/KEX: misc feature
LOCATION: (442)...(442)

OTHER INFORMATION: unknown amino
FEATURE:
NAME/KEX: misc feature
LOCATION: (475)...(475)

OTHER INFORMATION: unknown amino
FEATURE:
NAME/KEX: misc feature
LOCATION: (475)...(475)

OTHER INFORMATION: unknown amino
FEATURE:
NAME/KEX: misc feature
LOCATION: (475)...(475)

OTHER INFORMATION: unknown amino
FEATURE:
NAME/KEX: misc feature
COCATION: (5197)...(519)

OTHER INFORMATION: unknown amino
US-10-924-667-10
                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 96.4
Matches 726, Conservative
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Db 646 LHTVRAGSPSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSGLGEEE 705

Qy 721 PPALPSKLLSSGSCKADLGCRSYTDELHAVAPL 753

Db 706 PPALPSKLLSSGSCKADLGCRSYTDELHAVAPL 738
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Search completed: August 9, 2005, 11:54:38 Job time : 112.034 secs

Sequence 18, Sequence 18, Sequence 18

Sequence

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RIGMESQPFLANKFETDYFVKVVPFPSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISQYACHDQVAVTILWSPGALGIEFLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ADTCGWRMKAAARPRLCVANEGVGPASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 753;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 9;
US-10-616-788-2
US-10-104-047-3399
US-09-814-503-18
US-09-816-744-18
US-09-910-927-18
US-10-10-927-18
US-10-10-927-18
US-10-10-927-18
US-10-410-927-18
US-10-410-927-18
US-10-410-927-18
US-10-42-18-19
US-10-43-81-10
US-09-863-818A-10
US-09-912-157-12
US-09-912-157-12
US-10-717-282-12
US-10-717-282-12
US-10-717-282-12
US-10-717-282-12
US-10-717-282-12
US-10-713-348-16
US-10-616-788-16
US-10-616-788-19
US-10-616-788-19
US-10-616-788-19
US-10-616-788-19
US-10-616-788-19
US-10-616-788-19
                                                                                                                                                                                                                                                                                                                                                                                    US-10-033-522-1
US-10-207-655-107
US-10-742-161-10
US-10-742-372-10
US-10-646-308-4
US-10-918-084-1
US-10-918-161-2
US-10-742-372-2
US-09-863-818A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09912157
Fatent No. US20020165348A1
GENERAL INFORMATION:
APPLICANT: Presentl, Scott R.
APPLICANT: Gao, Zeren
TITLE OF INVENTION: Human Cytokine Receptor
FILE REFERENCE: 00-49
CURRENT APPLICATION NUMBER: US/09/912,157
CURRENT FILING DATE: 2001-07-23
NUMBER OF SEQ ID NOS: 13
SOUTHARR: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 3829;
100.0%; Pred. No. 0;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 718, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
CRGANISM: Homo sapiens
US-09-912-157-2
    US-09-912-157-2
                                 36
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Sequence 8, Appli
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Sequence 2, Appli
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Sequence 2, Appli
Sequence 5, Appli
                                                                                                                               (without alignments)
2696.128 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8,
Sequence 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2,
                                                                                                               August 9, 2005, 11:40:52 ; Search time 103.966 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT INEW PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/USO6_BNEW PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/USO6_BNEW PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/USO6_BNECOMB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/USO7_MEW PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/USO8_BNEW PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/USO8_BNEW PUB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/USO8_BUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/USO8_BUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/USO8_BUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/USO8_BUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/USO8_BUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/USO8_BUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/USO8_BUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/USO8_BUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/USO8_BUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/USO8_BUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/USO8_BUBCOMB.pep:*

19: /cgn2_6/ptodata/2/pubpaa/USO8_BUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/USO8_BUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/USO8_BUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/USO8_BUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/USO8_BUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/USO8_BUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/USO8_BUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/USO8_BUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/USO8_BUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/USO8_BUBCOMB.pep:*
                                                                                                                                                                                                         1 ADTCGWRMKAAARPRLCVAN.....CKADLGCRSYTDELHAVAPL
                       GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-717-282-2
US-09-912-157-5
US-09-912-157-8
US-09-912-157-8
US-10-717-282-8
US-10-717-282-8
US-10-608-449-2
US-10-608-449-2
US-09-809-567-2
                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-912-157-2
                                                                                                                                                                                                                                                                                      1752860 seqs, 390397842 residues
                                                                                 protein search, using sw model
                                                                                                                                                                       US-10-717-282-2_COPY_36_753
3829
                                                                                                                                                                                                                                                                                                                                                                                                                            Listing first 45 summaries
                                                                                                                                                                                                                                                      Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                 seq length: 0
seq length: 200000000
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                                      Copyright
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9

3829 3829 3819 3741 3741 3731 3731 3729 3725

100843371

Result No.

Gaps

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Sequence 3, Appli Sequence 3, Appli Sequence 9, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli

Sequence Sequence Sequence Sequence Sequence 1

Sequence 18, Appl Sequence 18, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 12, Appl Sequence 12, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 19, Appl Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli

Scoring table:

Searched:

Minimum DB Maximum DB

Database

Perfect score:

Sequence:

OM protein

Run on:

360 395

240 275 420

455

515

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61 TISQYACHDQVAVTILWSPGALGIEFLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFK 120
              276 NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 335
                                                                                                                                                                                                                                                                                                               RGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLM 480
                                                                                                                                                                                                                                                                                                                                                                                            DNLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFE 540
                                                                                                                                                                                                                                                                                                                                                                                                                                         541 KQFVPFHPPPLRYREPVLEKFDSGLVIANDVMCKPGPESDFCLKVEAAVLGATGPADSQHE 600
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APPLICANT: Kuestner, Rolf E.
APPLICANT: Guestner, Rolf E.
APPLICANT: Go. Zeren
TITLE OF INVENTION: Human Cytokine Receptor
FILE REFERENCE: 00-49
CURRENT APPLICATION NUMBER: US/09/912,157
CURRENT FILING DATE: 2001-07-23
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 753
TYPE: PRT
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99.7%; Pred. No. 0;
Live 0; Mismatches
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; Sequence 5. Application US/09912157
; Patent No. US20020165348A1
; GENERAL INFORMATION:
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Best Local Similarity 99.73
Matches 716; Conservative
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RIGMESQPFLNMKFETDYFVKVVPFPSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWK 215
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Publication No. US20040077052A1

GENERAL INPORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: Ruestner, Rolf E.
APPLICANT: Gao, Zeren
TITLE OF INVENTION: Human Cytokine Receptor
FILE REFERENCE: 00-49

CURRENT APPLICATION NUMBER: US/10/717,282

CURRENT FILING DATE: 2003-11-19

PRIOR APPLICATION NUMBER: US/09/912,157

PRIOR APPLICATION NUMBER: US/09/912,157

NUMBER OF SEQ ID NOS: 13

SSEQ ID NO
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100.0%; Score 3829;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 718; Conservative 0; Mismatches
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ORGANISM: Homo sapiens
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US-10-717-282-2
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APPLICANT: Kuestner, Rolf E.
APPLICANT: Goo, Zeren
TITLE OF INVENTION: Human Cytokine Receptor
FILE REFERENCE: 00-49
CURRENT APPLICATION NUMBER: US/09/912,157
CURRENT FILING DATE: 2001-07-23
NUMBER OF SEQ ID NOS: 13
SOFTWARE: RastSEQ for Windows Version 3.0
SEQ ID NO 8
LENGTH: 739
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98.1%;
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Best Local Similarity 98.1
Matches 704; Conservative
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99.7%; Pred. No. 0;
live 0; Mismatches 2;
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Publication No. US20040077052A1

GENERAL INFORMATION:
APPLICANT: Freenell, Scott R.
APPLICANT: Gao, Zeren
TITLE OF INVENTION: Human Cytokine Receptor
FILE REFRERENCE: 00-49
CURRENT APPLICATION UNDER: US/10/717,282
CURRENT FILING DATE: 2003-11-19
PRIOR APPLICATION NUMBER: US/09/912,157
PRIOR APPLICATION NUMBER: US/09/912,157
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 3.0
SSEQ ID NO 5.
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Matches 716, Conservative
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, ORGANISM: Homo sapiens
US-10-717-282-5
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| Sequence 2, Application US/10842006
| Publication No. US20040235104A1
| GENERAL INFORMATION:
| APPLICANT: Yang, Ruey-Bing
| TITLE OF INVENTION: A Novel Human SEF Molecule and Uses
| TITLE OF INVENTION: Therefor
| TITLE OF INVENTION: Therefor
| CURRENT APPLICATION NUMBER: US/10/842,006
| CURRENT PEPLICATION NUMBER: 60/469522
| PRIOR FILING DATE: 2003-05-08
| NUMBER OF SEQ ID NOS: 12
| SEQ ID NO. SEQ ID NOS: 12
| SEQ ID NO. SEQ ID NOS: 12
| LENTH: 739
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97.4%; Score 3731; D
Best Local Similarity 97.8%; Pred. No. 0;
Matches 702; Conservative 1; Mismatches
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ORGANISM: Homo Sapiens
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Publication No. US20040077052A1

GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: Gao, Zeren

TITLE OF INVENTION: Human Cytokine Receptor
FILE REFERENCE: 00-49

CURRENT APPLICATION NUMBER: US/10/717,282

CURRENT FILING DATE: 2003-11-19

PRIOR APPLICATION NUMBER: US/09/912,157

PRIOR APPLICATION NUMBER: US/09/912,157

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FastSEQ for Windows Version 3.0

FEQ. ID NO 80
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al Similarity 98.1%;
704; Conservative C
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ORGANISM: Homo sapiens
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Publication No. US20040235104A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: A Novel Human SEF Molecule and
TITLE OF INVENTION: Therefor
FILE REPREBNCE: MP103-071PLRM
CURRENT APPLICATION NUMBER: US/10/842,006
CURRENT FILING DATE: 2004-05-07
PRIOR FILING DATE: 2004-05-07
PRIOR FILING DATE: 2003-05-08
PRIOR FILING DATE: 2003-05-08
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: PASSEQ for Windows Version 4.0
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97.4%; Score 3729; D
Best Local Similarity 97.8%; Pred. No. 0;
Matches 701; Conservative 1; Mismatches
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US-10-842-006-4
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                     TISQYACHDQVAVTILWSPGALGIEFLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFK 120
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Publication No. US20040265834A1
GENERAL INFORMATION:
APPLICANT: Tainghua University
TITLE OF INVENTION: Human Interleukin-17 Receptor Like Molecule
FILE REPRENCE: 12003269C-US
CURRENT APPLICATION NUMBER: US/10/608,449
CURRENT PILING DATE: 2003-06-30
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 739
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Pred. No. 0;
1; Mismatches 1; Indels 14.
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al Similarity 97.8%;
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TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof
FILE REPERENCE: 010.7/36916A
CURRENT APPLICATION NUMBER: US/10/216,156
CURRENT FILING DATE: 2002-08-08
PRIOR APPLICATION NUMBER: US/09/809,567
PRIOR APPLICATION NUMBER: US/09/809,567
PRIOR APPLICATION NUMBER: US/09/809,816
PRIOR FILING DATE: 20001-01-128
PRIOR FILING DATE: 2000-01-16
PRIOR FILING DATE: 2000-01-16
PRIOR FILING DATE: 2000-01-16
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
TENNING TO 10 NOS: 17
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Pred. No. 0;
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; Sequence 2, Application US/09809567
; Patent No. US20020045213A1
; GENERAL INFORMATION:
    TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof
; FILE REFERENCE: 01017/36916A
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 08/724,460
; PRIOR PELING DATE: 2000-11-28
; PRIOR PELING DATE: 2000-13-16
; PRIOR PELING DATE: 2000-13-16
; NUMBER: OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver: 2.0
; SEQ ID NO 2
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TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof
FILE REFERENCE: 01017/39525
CURRENT APPLICATION NUMBER: US/10/616,788
CURRENT FILING DATE: 2003-07-10
PRIOR APPLICATION NUMBER: 09/809,567
PRIOR PELING DATE: 2001-03-15
PRIOR PILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 09/724,460
PRIOR PILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 06/189,816
PRIOR PILING DATE: 2000-03-16
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTIN VOY: 2.0
SEQ ID NO 2
LENGTH: 738
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   700; Conservative
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ORGANISM: Homo sapiens
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                                                                     62 ISQYACHDQVAVTILWSPGALGIEFLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFKR
                                                                                                                            263 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAMAITVPLVVISAFATLFTVMCR
                                                                                                                                                                                                                                                                                                                                                           443 GSGKGELFLVAVSAIAEKURQAKQSSSAALSKFIAVYFDYSCEGDVFGILDLSTKYRLMD
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                                                     2 DICGWRMKAAARPRLCVANEGVGPASRNSGLYNIIFKYDNCTTYLNPVGKHVIADAQNII
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                         Gaps
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; Publication No. US20030236392A1
; GENERAL INPORMATION:
    APPLICANT: HELIX RESEARCH INSTITUTE
    TILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; WINBER OF SEQ ID NOS: 4096
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3399
Length 738
                         Indels
DB 15;
                         1;
                            1; Mismatches
Score 3725;
Pred. No. 0;
97.3%;
97.8%;
                            Conservative
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ORGANISM: Homo sapiens
Query Match
Best Local Similarity
Matches 700; Conserv
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US-10-104-047-3399
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FILING DATE: 2000-02-18
APPLICATION NUMBER: US PCT/US99/31274
FILING DATE: 1999-12-30
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           Watanabe, Colin K.
Williams, P.Mickey
Wood, William I.
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                                                                                                                                                                                   ALGIEFLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFKRTGMESQPFLNMKFETDYFV 150
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                                                                                                                                                                                                                           KVVPFPSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKPRNLNISQHGSDMQVSFDHA 200
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                                                                                                                          90
                                                                                                                VMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQQENIYSHLDEESSESS
                                                                                             21 EGVGPASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVTILWSPG
                                                               Gaps
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                              DB 15; Length 728;
                                                             Indels
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                              96.8%; Score 3708; I
99.7%; Pred. No. 0;
ive 1; Mismatches
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Patent No. US2002017188A1
GENERAL INFORMATION:
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Grimaldi, J. Christopher
Gurney, Austin L.
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VanLookeren, Menno
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Hillan, Kenneth J.
Hymowitz, Sarah G.
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Filvaroff, Ellen
                                             al Similarity 99.7
696; Conservative
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Goddard, Audrey
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US-10-104-047-3399
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Best Local
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APPLICANT: WILLIAMS, P. MACKAY
APPLICANT: WILLIAMS, P. MACKAY
APPLICANT: WILLIAMS, P. MACKAY
APPLICANT: WOOG, WILLIAM: P. HOROCOGNE POLYPEPTIDES AND THERAPEUTIC USES THEREOF
TILE OF INVENTION: IL-1 THOROCOGNE: US 00/16/05
CUTRENT PELLON HUMBER: 1001-06-05
PRIOR PEPLICATION NUMBER: 106 00/25, 646
PRIOR APPLICATION NUMBER: 106 00/25, 646
PRIOR APPLICATION NUMBER: 106 00/25, 646
PRIOR APPLICATION NUMBER: 106 00/24, 937
PRIOR FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: 106 00/24, 401
PRIOR PELLING DATE: 2000-01-11
PRIOR PELLING DATE: 2000-01-11
PRIOR PELLING DATE: 2000-01-11
PRIOR PELLING DATE: 2000-01-11
PRIOR PELLING DATE: 1000-01-11
PRIOR PEPLICATION NUMBER: 106 60/13, 201
PRIOR PEPLICATION NUMBER: 106 60/13, 201
PRIOR PEPLICATION NUMBER: 106 60/13, 201
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APPLICATION NUMBER: US PCT/USOO/05841
PILLING DATE: 2000-03-02
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APPLICATION NUMBER: US PCT/US00/23328
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APPLICATION NUMBER: US PCT/US00/30873
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APPLICATION NUMBER: US PCT/US00/15264
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US-09-816-744-18
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                                                                                                                                                                                                                               SQPFLNMKFETDYFVKVVPFPSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKPRNLN 185
                                                                                                                                                            NYKHKGGGRGSGKGELFLVAVSAIAEKIRQAKQSSSAALSKFIAVYFDYSCEGDVPGILD
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                                                                                                                             Gaps
                                                                                                                             14;
                                                                                                                             Indels
                                                                                                           Length
                                                                                                                            8;
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                                                                                                          Score 3703; DE Pred. No. 0; 2; Mismatches
PRIOR APPLICATION NUMBER: US PCT/US99/10733
PRIOR FILIG DATE: 1999-05-14
PRIOR APPLICATION NUMBER: US PCT/US99/05028
PRIOR FILING DATE: 1999-03-08
NUMBER OF SEQ ID NOS: 39
SEQ ID NO 18
LENGTH: 728
                                                                                                           96.7%;
                                                                                                                                Conservative
                                                                    TYPE: PRT
ORGANISM: Homo Sapien
US-09-874-503-18
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Sequence 18, Application US/09816744 Publication No. US20030003546A1 GENERAL INFORMATION:

RESULT 15 US-09-816-744-18

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APPLICANT: Yansura, Daniel
TITLE OF INVENTION: 11-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
FILE REFERENCE: P1381R1C1P2 (US)
FURRENT APPLICATION NUMBER: US/09/816,744
CURRENT FILING DATE: 2001-03-22
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 39
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Pred. No. 0;
                                                           Godowski, Paul
Grimaldi, Christopher
Gurney, Austin
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Best Local Similarity 96.7%;
Matches 702; Conservative 2
                                                                                                                                                                                                                Watanabe, Colin
Williams, P.Mickey
Wood, William
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Hillan,Kenneth
Tumas,Daniel
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Filvaroff, Ellen
                                        Goddard, Audrey
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ORGANISM: Homo Sapien
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Search completed: August 9, 2005, 11:54:41 Job time: 106.966 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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(C,Accession: T42695
(R;Bloecker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, Bubmitted to the Protein Sequence Database, November 1999
A;Reference number: Z22230
A;Accession: T42695
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-564 <AAA>
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                          hypothetical protein DKFZp434N1928.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                     1 HPFFFRTRACDLLLQPDNLACKPFWKPRNLNISQHGSDMQVSFDHAPHNFGFRFFYLHYK
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A;Experimental source: adult testis; clone DKFZp434N1928
C;Genetics:
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Matches 563; Conservative
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Sat Aug 13 10:40:56 2005

Db 704 DELKEKFAAKRDLEVEVLDSEDVKLLEDVKCAF Qy 602 QHGGLDQDGEARPALDGSAALQPLL-HTV ::	RESULT 3 T30113 hypothetical protein F56D1.2 - Caenorhabditis	C; Species: Caenorhabditis elegans C; Date: 15-Ot-1999 #sequence_revision 15-Ott- C; Accession: T30113 R; Chissoe, S.; Wilson, R. R; Chissoe, S.; Wilson, R. A; Description: The sequence of C. elegans cost	A,Accession: T30113 A,Status: preliminary; translated from GB/EMBL/A,Molecule type: DNA A,Molecule type: DNA A,Residues: 1-718 <chi>A,Residues: 1-718 <chi>A,CHI>A,CHOSS.references: UNIPROT:Q10128; EMBL:U39997</chi></chi>	C;Genellos: A;Gene: CESP:F56D1.2 A;Gene: CBSP:F56D1.2 A;Introns: 93/1; 121/2; 163/3; 459/1; 5: C;Superfamily: Caenorhabditis elegans h	Query Match 3.3%; Score 126.5; Best Local Similarity 20.6%; Pred. No. 0.0 Matches 89; Conservative 68; Mismatches	Qy 280 VAITVPLVVISAFATLFTVMCRKKQQE	Qy 334 RPKVFLCYSSKDGQNHMAVVQCFAYFLQDFCGC : : : : : : Db 414 FVKYMIVYAD-DNDLHTDCVKKLVENLRNCAS	Qy 394 SQFIIVVCSKGMKYFVDKKNYKHKGGGRGSGKC	Qy 454 FIAVYPDYSCEGDVPGILDLSTKYRLMDNI :	Qy 511 NYFRSKSGRSLYVAICNMHQFIDEEPDWFE :	OY 562 DSGLVLNDVMCKPGPESDFCLKVEAAVLGATGE :	Qy 622 LQPLLHTVKAGSPSDMPRDSGIYDSSVPSSF 	Qy 680 GLGEEEPPALPSK 692 Db 707 GEDPKTIVVK 716		Celomere-associated recylitke melicase - smuc C;Species: Ustilago maydis (corn smut) C;Date: 11-Jun-1999 #sequence_revision 11-Jun C;Accession: T09081	R;Sanchez-Alonso, P.; Guzman, P. Genetics 148, 1043-1054, 1998 A;Title: Organization of chromosome end
Db 421 GPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAALQPLLHTVKAGSP 480 Qy 635 SDMPRDSGIYDSSVPSSELSLPLMRGLSTDQTETSSLTESVSSSGLGEEEPPALPSKLL 694	Qy 695 SSGSCKADLGCRSYTDELHAVAPL 718 	T27282 T27282 hypothetical protein Y64G10A.e - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: L3-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004	R.Ainscough, R. submitted to the EMBL Data Library, September 1999 A.Reference number: Z20336 A.Reference number: T27282 A.Status: preliminary, translated from GB/EMBL/DDBJ	A,MOLGOULE type: DNA A,Residues: 1-646 <wil> A,Cross-references: UNIPROT:Q9NA64; EMBL:AL110498; PIDN:CAB54470.1; CESP:Y64G10A.e A,Experimental source: clone Y64G10A</wil>	. G. Generic CESP: Y64G10A. e A;Gene: CESP: Y64G10A. e A;Introns: 106/1; 198/3; 261/1; 301/3; 386/1; 416/2; 475/1; 510/3; 580/2; 815/3 C;Superfamily: Caenorhabditis elegans hypothetical protein Y64G10A. e	Query Match 4.5%; Score 170.5; DB 2; Length 846; Best Local Similarity 21.4%; Pred. No. 3.7e-05; Matches 141; Conservative 82; Mismatches 225; Indels 211; Gaps 37;	Qy 64 QYACHDQVAVTILWSPGALGIEFLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFKRTG 123	Qy 124 MESQPFLNMKFETDYFVKVVPFPSIKNESNYHPFFFRTRACDLLLQPDNLAC-KPFWKPR 182	Qy 183 NLNISQHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTETTSCLLQNV 242 	Qy 243 SPGDYIIELVDDTNTTRKVMH-YALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVM 299 Db 416	Qy 300 CRKKQQENIYSHLDEESSESSTYTAALPRERLRPRVVFLCYSSKDGONHMVVQCFAYF 359 Db 446 NNKKKASNIHLINENPAFS-HSGSIPL-ILKQSISVLIVY-SHDSAQHEAAVLAFAEL 500	Qy 360 LQDFCGCEVALDLWEDFSLCREGOREWVIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGG 419	QY 420 GRGSGKGELFLVAVSAIABEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILDLSTKY 477	Qy 478RLMD-NLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAI 525	Qy 526 CNMHQFIDBEPDWPEK	Qy 555 EPVLEKF

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stilago maydis: recQ-like helicase motifs a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; DB 2; Length 718;
.096;
es 165; Indels 111; Gaps 20;
                                                                                                                                                                                                                                                                                                                                                                                   97; PIDN: AAA81100.1; CESP: F56D1.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DENIYSHLDEESSESSTYTAALPRERLRP 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCEVALDLWEDFSLCREGOREWVIQKIHE 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |: || : : ||: :|
SCDPVFDLEKLITAEQIVPSRWLVDQISS 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KGELFLVAVSAIAEKLRQAKQSSSAALSK 453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             || : ||: :| |
|QFAQLTAFI.HNVEH-----TERA 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEKOFVP-----FHPPPLRYREPVLEKF 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | :: | | | | :: ||:
|LETRWKPKDELAALH---LKRQSPVIVPI 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPADSQHESQHGGLDQDGEARPALDGSAA 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | : : | |: |
VPPQALVDSD----DBD------DVD 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SELSIPLMEGLSTDQTETSSLTESVSSSS 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |------SDSESDSSESESDNE 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VRNI -----ALTE 413
APGP----IHVEPTEPEVLEPAEEPMEE 758
                                TVKAGSPSDMPRDSGIYDSS-VPSSELS 654
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smid F56D1.
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KURQAKQSS-SAALSKFIAVYFDYSCEGDVPGI------LDLSTKYRLMDNLPQ 485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        235 TSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVIS-AFA 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       294 TLFTVMCRKKQQENIYSHLDEESSESSTYTAALPRERLRPRPKVFLCYSSKDGQNHMNVV 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QCF---AYFLQDFCGCEVALDLWEDFSLCREGQREWV----IQKIHESQFIIVVCSKGMK 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---AEKLRQAKQSSSAALSK 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           454 FIAVYFDYSCE-----GDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTRQG 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                673 EIAVYHDLTARENLAFFCKIYGLKGEELKHR-MESTLÖLV------GLEE-----RON 718
                                                                                                                                                                                                                                                                                                                                   424 ARDFKVYECESCEGCPFKPECTKARGNROVHYNPVY------EELKAKOHOKLK 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   524
                                                                                                                                                                                                                                                                                                                                                                           183 NINISQHG-----SDMQVSFDHAPHNFGFRFFYLHYKCLKHEGPFKRKTCKQEQTTET 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                       EFLKGFRVILEELKSEGR------QCQQL--ILKDPKQLNSSFKRTGMESQPFLNMKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----SRFYVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     613 MFIEKGEMVGLLGPNGAGKSTTISMISŚLÍQPTSGDVLIKGGSIHKQSKAIRŚILGVVPQ
                                                                                                                                                                ALKESGL------PLPKTLIADAGYGSESNYVAMADELFETLIPS-----
                                                                                                                         26 ASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNITISQY-ACHDQVAVTILWSPGALGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                     Indels 215;
                                            Length 901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: T17212
R;Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann,
submitted to the Protein Sequence Database, September 1999
A;Reference number: Z18723
A;Accession: T17212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 110; DB 2; Length 535; Pred. No. 1.3; 42; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             ----seegrtlyokrktdvesvfghvkonlgfrklhlrgk-----
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A;Residues: 1-488;489-535 <POU>
A;Cross-references: UNIPROT:Q9NTU6; EMBL:AL117401
A;Experimental source: adult testis; clone DKF2p434P211
A;Note: the cDNA sequence contains a -1 frameshift near
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein DKFZp434P211.1 - human (fragments)
                                               3.0%; Score 116.5; DB 2;
19.6%; Pred. No. 0.85;
tive 76; Mismatches 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              407 YFVDKKNYKHKGGGRGSGKGELFLVAVSAI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        || | | : : | | : |:
525 KRATVDRRSKEPKNTNQHKNREN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               508 SRRNYFRSKSGRSLYVAICNMHQ---FIDEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.9%;
Best Local Similarity 23.5%;
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Best Local Similarity
Matches 112; Conserv
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          A;Gene: BH1054
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------RLMDNLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFRS 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               332 SQESGRAGRDGMPAESILLAGPQLDDRAP-ASGKASSAEKGKVAPG---ADKEAMQLYRS 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       516 KSGRSLYVAICNMHQFIDEEPDWFEKQFVPFHPPPLRYREPVLEKFDSGLVLNDVMCKPG 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PESDFCLKVEAAVLGATGPADSQH---ESQHGGLDQDGEARPALDGSAALQPLLHTVKAG 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPSDMPRDSGIYDSSVPSSE-LSLPLMEGLSTDQTETSSLTESVSSS---SGLGEEEPPA 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------GSSHPSSHGSSHPSIHGSSHPSIHGSS-HPSIHGSGQHGGQRRKQQPD 510
                                                                                                                                                                                                                                                                                                                        233 ETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAV----AITVPL-- 286
                                                                                                                                                                                                                                                                                                                                               ||| :| |: : :| | : : :| | | || || || ETTILILPTVALRANMLAKLDVMN----IRYHVWQP-GSKKAAPIVLVSTBAAITLAFKE 131
                                                                                                                                                                                                                                                                                                                                                                                                       287 ------VVISAFATLFTVMCRKKQQENIYSHLDEESSESSTYTAALP---- 327
                                                                                                                                                                                                                                                                                                                                                                                                                                 --RERLRPRPKVF-----LCYSSKDGQNHMNVVQCF-AYFLQDFCGCEVALDLWEDF 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FISHNKLTKPLIVRESTNRSNLCYSVRTAEHRMSGMTCYDAVRVVD--ECRARTDIW--- 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     377 SLCREGOREWVIQKIHESOFIIVVCSKGMKYFVDK-----KNYKHKGGGRGS----- 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----NGORD------RIIVYCTS--KELVARLAEMLGCAAYSSESGSEADKAAIIQ 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----GKGELPLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGIL--DLSTKY 477
A;Reference number: Z16557; MUID:98198830; PMID:9539423
A;Accession: T09081
A;Statule: prefilminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-757 <SAN>
A;Cross-references: UNIPROT:013399; EMBL:AF030885; NID:92642221; PID:92642222
A;Experimental source: strain FB2
C;Genetics:
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                                                                                                                                                                                                                                                                                 190;
                                                                                                                                                                                                                                       Length 757;
                                                                                                                                                                                                                                    / Match 3.1%; Score 117; DB 2; Length 75; Local Similarity 20.4%; Pred. No. 0.6; Conservative 56; Mismatches 187; Indels
                                                                                                                                                                                                                                                                                 Matches 111; Conservative
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C, Keywords: DNA binding
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Best Local 9
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Cjacession: T04661
RjBevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Jesse, T.; Heijnen, L.; Vos, P.; Mewes, submitted to the Protein Sequence Database, July 1998
AjReference number: 215381
AjAccession: T04661
AjMolecule type: DNA
AjResidues: 1-917 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58/2; 93/1; 274/3; 340/3; 373/3; 395/1; 437/3; 536/1; 624/2; 665/3; 685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----ALTPVY------LQVSLVDIEBANVLYTKHIASDICPGIISLQFE 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                485 SCIVQGFEKNVLVVAMRDSSVFA-LDSDTGNMIGTNMIKPK-----KPFKVLYMQILDGK 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      348 NHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQKIHESQFIIVVCS---- 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QAKQS-----SSAALSKFIAVYFDYSCEGD------VPGILDLSTKYRLMDNL 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----HPPPLRYREPVLEKFDSGL 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FLNMKFETDY-----FVKVVPFPSIKNESN---YHPFF-----FRTRACDLLLQPDNL 173
                                                                                                                                                            hypothetical protein F8D20.70 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----KGMKYFVDKKNYKHKG------KGRGSGKGELFLVAVSAIAE----KLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPASR-----NSGLYNITFKYDNCTTYLNPVGKHV---IADAQNI--TISQYACHDQVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACK----PFWKPR-NLNISQHG------SDMQVSFDHAPHNFGFRFFYLHYKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216 KH-----EGPFKR-----KTCKQEQTTETTSCLLQNVSP------GDYIIELVDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----VMCRKKQQENIYSHLDBESSESSTYTAALPRERLRPRPKVFLCYSSKDGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.9%; Score 110; DB 2; Length 917; Best Local Similarity 18.1%; Pred. No. 2.9; Matches 154; Conservative 124; Mismatches 281; Indels 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C, Superfamily: Arabidopsis thaliana hypothetical protein F8D20.70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     255 TNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFT
                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UMIPROT:081789; EMBL:AL031135
A;Experimental source: cultivar Columbia; BAC clone F8D20
|| |: || : | : | 447 VPIVPPSQQAKPLRKDRSAEET 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               538 WFEKQFVPF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Genetics:
A;Map position: 4
A;Introns: 13/3; 58
A;Note: F8D20.70
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C.Species: Mus musculus (house mouse)
C.Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C.Accession: 14929
R.Tellam, J.T.; McIntosh, S.; James, D.E.
J. Biol. Chem. 270, 5857-5863, 1995
A.Title: Molecular identification of two novel Munc-18 isoforms expressed in non-neurona
A.Reference number: 149238; MulD:95197608; PMID:7890715
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A;Molecule type: mRNA
A;Residues: 1-592 <RES>
A;Cross-references: UNIPROT:Q60770; EMBL:U19521; NID:g642027; PIDN:AAA69913.1; PID:g6420
C;Genetics:
A;Gene: munc-18c
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                                                                        VLGATG-PADSQHESQHGGLDQDGEARPALDGSAALQPLLHTVKAGSPSDMP-----RD 640
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                                                                                                                                                                                                                                                                                                                   268 ATGASGLPAVSKAPS----MDAQQETHKSQDCLGLLDPLASA--AGVPSTAPMSGKKHRP 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 IMLLDEPTTKLLSSCCKATDLLEEGITVIENİYKOREPVRQMKALYF-----ISPTPK 86
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OY 431 VAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILDLSTKYR 478 :	0y 617 DGSAALOPLAHTVAGASBGANFRAGAINSSVDSELSLPLANGIGS 662 DE SES DCTPLHINGLALCOVADRAILAPENTING,
	PSESUIT 9 593762. 5937

THALPREKLARPREKUFLCYSSKDGONHANVOCPAYFLODFC-GCE 367	HEGPFRRKTCK -GFSLHKGPSLHKDAHINTINLFI
Db 716 CNLIGKGNVIVOWKLYNYIFNPVLQRGVELVHHCQQLSITSA 757 Oy 121 RIGMESOPFLNMKFET-DYFVKVVPFPSIKNENYHPF 157	
	Qy 481 DNLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFRSKGGRSLYVAICNMHQFIDEE 535 Db 3535 DTCPQFCSSHSMPDVQEHVKDGPRAHAYKREEGYMLDDSHCVVSDSEAYHLGQEE 3589 Qy 536 PDWFEKQFVPFHPPPLRYREPVLEKFDSGLVLNDVMCKPG 575 Db 3590 TDWFDKPRDARSDRFRHHGGHTVSSQKRGPARHSYHDYDEPPEEGLWPHDEGG 3643

OV 576 PESDFCLKVEAAVLGATGPADSOHESOHGGLDQDGEARP- 614	q	::: ::: :::: ::::::::::::::::::::::
3644	ò	RDHGLQEPGQHTRQGSRRNY
Qy 615ALDGSAALQPLLHTV 629	QΩ	571 VFRINSNIRQLCYMCHRRCTGLIFYEGYRRNATYYVHSNRSTHRM 616
DD 3692 PQASPAPAMQKKGQPGYPSSADYSQSSRAPSAYHHASESKKGSRQAHTGPSALQPKADTQ 3751	δδ	524 ALCNM 528
Qy 630 KAGSPSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSGLGEEEPPAL 689	qa	617 IFCSL 621
Db 3752 AQPQMQGRQAAPGPQQSQPPSSRQTPSGTASRQPQTQQQQQQQQQQQQQQQGAPQQA 3808	RESULT 14	
Oy 690 PSK 692	T30851 lysosom	al trafficking regulator, long splice form - mouse
Db 3809 PSQ 3811	N;Alter C;Speci C:Date:	nate names: Delge protein nomolog es: Mus musculus (house mouse) 22-Oct-1999 #sequence revision 22-Oct-1999 #text change 09-Jul-2004
RESULT 13 D86477	C, Acces R, Barbo	sion: T30851 sa, M.D.F.S.; Tchernev, V.T.; Kingsmore, S.F.
protein F1504.27 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ar cress) C:Date: 02-Mar-2001 #sequence revision 02-Mar-2001 #text change 09-Jul-2004	submitt A;Descr A;Refer	submitted to the kmin nata hibrary, september 1990 A;Description: Two bg or not two bg? Longest isoform of mouse Lyst (beige) gene. A;Reference number: 220903
C; Accession: D86477 R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,	A; Acces A; Statu	sion: T30851 s: preliminary; translated from GB/EMBL/DDBJ n- preliminary; translated from GB/EMBL/DDBJ
•	A;Resid A;Cross	Afficiency
Nature 400, 010'020, 2000 Ayduthors: Hunter, J.L.; Johkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,	A; Exper C; Genet	imental source: strain C57BL/6J ics:
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,	A, Gene: A, Map p	A;Gene: Lyst A;Map postition: 1
<pre>ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, K.W. A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.</pre>	C, Ney wo	Match Ma
A;Reference number: A86141; MULD:21016/19; FMLD:11130/12 A;Accession: D86477 A;Gratus: prejiminary	Best Lo	154; Conservative 99; Mismatches 275
	ò	16 LCVANEGVGPASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNITI 62
A;Cross-references: UNIPROT:Q9LQF8; GB:AE005172; NID:g8778345; PIDN:AAF79353.1; GSPDB:GN C;Genetics:	qq	658 LCGAGPTSGLPSPSYRFQGILPSSGSEDLLWKWDALEAYQSFVFQEDRLHNIQI 711
A;Gene: P1504.27 A;Map position: 1	ò	63 SQYACHDQVAVTILWSPGALGIEFLKGFRVILBELKSEGRQCQQLILKDPKQLN 116
Query Match 2.8%; Score 106.5; DB 2; Length 638;	qa	712 ANHICNLLQKGNVVVQWKLYNYIFNPVLQRGVELVHHCQQLSIPS 756
vative 63	ò	
ALGIEFLKGFRVILEELKSEGRQCQQLILKDPKQLNSS	셤	AQTHMCSQLKQYLPQEVLQIYLKTLPVLLKSRVIRDLFLSCNGVNHIIBLNYLDGIR
DIKYGQYSCHLQDCFYVVHSKCATHENVWDGKELEWEIESDETEDISP	ð 1	155 -HPF-PFRTRACDLLLQPDNLACKPFWKERNLNLSQHGSSMQVSFUHAFHNFGFRFILM 212
119	3 8	VKT KHEGDEKEKTICKOEGITETISCIJONVSPGDX I I ELVDDINITEKVMHYALKEVHSP
	; 쉼	
365 HQFYHCKKCNYSLHEVCAGLSRKLDHALHNHTLILSPSPGKFCCSACSREST	ò	273 WAGPIRAVAITVPLVVISAFATLFTVMCRKKQQENIYSHLDBESSESSTYTAALPRERLR 332
Qy 232 TETTSCLLONVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISA 291	qq	894INTINIFICVAFLCVSKEADSDRESANESEDISGYDSPPSE 934
Db 417 GFSYICSNKGCQDFVLDVRCISVLEYFIHRSHEHPFIFISTS 457	δ	CGCEVALDLWEDFSLCREGOREWV-
QY 292 FATLFTVMCRKKQQENIYSHLDEESSE-SSTYTAA-LPRERLRPRPKVFLCYSSKDG 346	Dβ	
Db 458 YNSKDEILCKVCKKRCLGAHLQCTLCEFTMCYSCAIIPDEIHYKFDKHPLTLSCGESAD- 516	ð	388 -IQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGGRGSKGELFLVAVSAI 436 : : :
Qy 347 QNHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQKIHESQFIIVVCSKGMK 406	qq	
Db 517NTYWCEVCEKQLDPREWFYTCNKCCITIHLHCIFGSS 553	ζō	437 AEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMDNLPQ 485
Qy 407 YFVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGD 466	qa	1028YPELTLKGDVSSATAPDLGFLRKSADSVRGFQSQPVLPT 1066

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RESULT 15
JC6033
dead ringer nuclear protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 13-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession. JC6093
R;Gregory, S.L; Kortechak, R.D.; Kalionis, B.; Saint, R.
Mol. Cell. Biol. 16, 792-799, 1996
A;Title: Characterization of the dead ringer gene identifies a novel, highly conserved f
A;Reference number: JC6093
A;Accession: JC6093
A;Accession: JC6093
A;Accession: JC6093
A;Accession: JC6093
A;Accession: UC6093
A;Cross-references: UNIPROT:Q24573; GB:U62542; NID:g1480739; FIDN:AAB05771.1; PID:g14807
C;Genetics:
A;Gene: dri
C;Keywords: DNA binding; embryo
                                       1067 SAEQIVATE---SVPGE----RKAFMSQQSETSLQSIRLLESLLD------IC 1106
                                                                                                           | :: || |:|
1107 LHSARACQQKMELELPSQGLSVENILCELREHLSQSKVABTELAKPLFDALLRVALGNHS 1166
                                                                                                                                                                                          1227 TQDDGV---ELN-PEAEGFS-GSIVSNNLLENLTH----GELIYPEICMLGLNLLSASKA 1277
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                                                                                 --PGPESDFCLKVEAAVLG 590
                                                                                                                                                                    591 A-TGPADS----QHESQHGGLDQDGEARPALDGSAALQPLLHTVKAGSPSDM---PRDSG 642
                                                                                                                                                                                                                                                       643 IYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSSGLGE---EEPPALPSKLLSSGSC 699
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486 LCSHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFEKQFVP 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    370 LDLWEDFSL--CREG-----QREW--VIQKIHESQFI----IVVCSKGMKYF----VDK 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       434 SAIAEKLR-QAKQSSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMDNLPQLC---- 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  521
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20.4%; Pred. No. 7.1;
trive 56; Mismatches 157; Indels 162;
                                                                                 FHPPPLRYREPVLEKFDSGLVLNDVMCK---
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Best Local Similarity 20.4*
Matches 96; Conservative
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Search completed: August 9, 2005, 11:49:57 Job time : 31.7981 secs

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QDFCGCEVALDLWEDFSLCREGREWVIOKIHESOFIIVVCSKGMKYFVDKKNYKHKGGG 420
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(c) 1993 - 2005 Compugen Ltd
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI TaxID=9606,
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97.5%; Score 3735; DB 2; Length 739;
Best Local Similarity 97.9%; Pred. No. 7.8e-275;
Matches 703; Conservative 0; Mismatches 1; Indels 1
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SEQUENCE FROM N.A.

Gaibert J.M., Gorman D.M.;

Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AF458067; AAM77571.1; -.

GO; GO:0014689; Firansmembrane receptor activity; IEA.

GO; GO:0004889; Firansmembrane receptor activity; IEA.

INCEPPO; IRRO0157; TIR.

SEQUENCE 739 AA; 82440 MW; 1670803DD0CD0F17 CRC64;
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06NZR7
06RN9
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06CGD7
0758M4
06PFW1
06PFW1
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562 KQFVPFHPPPLRYREPVLEKFDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHE 621
                                                                            301 RKKQQENIYSHLDEESSESSTYTAALPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAYFL 360
                                                                                                                                                                    RGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLM 480
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PRNINISQHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCEQEQTTEMTSCLLQ 261
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PubMed=14742070; DOI=10.1073/pnas.0307952100;
Preget E., Ziv I., Shabtay A., Sher I., Tsang M., Dawid I.B.,
Altuvia Y., Ron D.;
"Alternative splicing generates an isoform of the human Sef gene with
Alternative splicing generates an isoform of the human Sef gene with
altered subcellular localization and specificity.";
Proc. Natl. Acad. Sci. U.S.A. 101:1229-1234(2004).
EMBL, AY489047; AAS15051.2;
GO; GO:0016020; C:membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005057; TIR.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Matches 696; Conserv
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Whomdel=1598313; DOI=10.1074/jbc.M306936200;

Xiong S., Zhao Q., Rong Z., Huang G., Huang Y., Chen P., Zhang S.,

Liu L., Chang Z.;

"Nsef inhibits PC-12 cell differentiation by interfering with Rasmitogen-activated protein kinase MAPK signaling.";

"Biol. Chem. 278:50273-50282(2003).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Xiong S.Q., Huang G.R., Zhao Q.H., Chen P.L., Rong Z.L.,
Chen Y., Liu L., Fu X.Y., Chang Z.J.;
Submitted (MAE-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF494208; AMM74077.1;
Genew; HGNC:17616; IL17RD.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Interleukin 17 receptor-like protein long form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cch 97.4%; Score 3731; DB 2; s1 Similarity 97.8%; Pred. No. 1.6e-274; 702; Conservative 1; Mismatches 1;
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                                                                                                                              7 RMKAAARPRLCVANE-GVGPASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNITISQY
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
GO; GO:0004888; F:transmembrane receptor activity; IEA
                                4AD9D3F6B1C78C26 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Transmembrane protein (Interleukin 17 receptor-like
                                                            / Match
Local Similarity 96.7%; Pred. No. 2.1e-272;
Les 702; Conservative 2; Mismatches 8;
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                 InterPro; IPR000157; TIR. SEQUENCE 728 AA; 81310 MW;
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                                       KVVPFPSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKPRNLNISQHGSDMQVSFDHA
                                                                                                      PHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTEMTSCLLQNVSPGDYIIELVDDTNTTRK
                                                                                                                                                                    FDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSA
                                                                                    PHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTETTSCLLQNVSPGDYIIELVDDTNTTRK
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                    KVVPFPSIKNESNYHPFFFRTRACDL1LQPDNLACKPFWKPRNLNISQHGSDMQVSFDHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORFNames=UNQ6115;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGEEEPPALPSKLLSSGSCKADLGCRSYTDELHAVAPL 718
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Last sequence update)
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Genome Res. 13:2265-2270(2003).
EMBL, AYSS8774; AAQ89134.1; -
GO; GO:0016020; C:membrane; IEA.
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                                                  SECUENCE FROM N.A.

MEDLINE=21959295; PubMed=11960706; DOI=10.1016/S0925-4773(02)00018-7;
Lin W., Furthauer M., Thisse B., Thisse C., Jing N., Ang S.-L.;
"Cloning of the mouse Sef gene and comparative analysis of its
expression with FQF8 and Spry during embryogenesis.";
Mech. Dev. 113:163-168(2002).
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Liu L., Chang Z.;
MsSef inhibits PC-12 cell differentiation by interfering with Rasmitogen-activated protein kinase MAPK signaling.";
J. Biol. Chem. 278:50273-50282(2003).
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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L. Submitted (MAR-2002) to the EWBL/GenBank/DDBJ databases.

E. BML, AR459444;

EMBL, AR494210;

R. EMBL, AR494210;

R. EMBL, AR494210;

R. GO; GO:001021;

R. GO; GO:000570;

R. GO; GO:0005676;

R. GO; GO:0005676;

R. GO; GO:0008670;

R. GO; GO:0008709;

R. GO; GO:0008709;

R. GO; GO:0008709;

R. GO; GO:0008709;

R. GO; GO:0008709;

R. InterPro; IPR007087;

R. InterPro; IPR007087;

R. InterPro; IPR007087;

R. InterPro; IPR07087;

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84.9%; Pred. No. 6.8e-236;
ive 37; Mismatches 51;
                                                                                                                                                                                                           STRAIN=BALB/c;
PubMed=12958313; DOI=10.1074/jbc.M306936200;
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les 612; Conservative
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                 NCBI_TaxID=10090;
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                                                                                    EKQFVPFHPPPLRYREPVLEKFDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQH 599
                                                                                                                                                                        -- ESQHGGLDQDGEARPALDGSAALQPLLHTVKAGSPSDMPRDSGIYDSSVPSSELSLPL 657
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                           DNLPQLCSHLHSRDHGLQEP-GQHTRQGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 27, Last sequence update)
05-UTL-2004 (TrEMBLrel. 27, Last annotation update)
Interleukin 17 receptor-like protein short form (Hypothetical protein
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EMBL; AR934211; AAM74080.1; --
EMBL; AL833913; CAN38769.1; --
EMBL; AC016020; C:membrane; IEA.
GO; GO:0016020; F:transmembrane receptor activity; IEA.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PubMed=12598313; DOI=10.1074/jbc.M306936200;
Xiong S., Zhoo Q., Rong Z., Huang G., Huang Y., Chen P., Zhang Liu L., Chang Z.;
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99.8%; Pred. No. 4.9e-232;
live 0; Mismatches 1;
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Homo sapiens (Human)
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Hypothetical protein; Receptor.
SEQUENCE 595 AA; 66846 MW; 7
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TISSUE=Testis;
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                    515 SKSGRSLYVAICNMHQFIDEEPDWFEKQFVPFHPPPLRYREPVLEKFDSGLVLNDVMCKP
                                                                                                                                                                                                                                                                                            361 SKSGRSLYVAICHMHQFIDEEPDWFEKQFVPFHPPPLRYREPVLEKFDSGLVLNDVMCKP
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                                                                                   QFIIVVCSKGMKYFVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKF
                                                                                                                                                                           IAVYFDYSCEGDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFR
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
10-0CT-2003 (TrEMBLrel. 25, Last annotation update)
For signaling antagonist SEF.
Gallus gallus (Chicken).
Eukaryota; Metazoa Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
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PKVFLCYSSKDGQNHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQKIHES
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Matches 533; Conservative
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                                                                                                                                                                                                           QQENIYSHLDEESSESSTYTAALPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAYFLQDF
                                  CGCEVALDLWEDFSLCREGOREWVIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGGRGS
                                                                                                                                                                                      GKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMDNL
                                                                                                                                                                                                                                                                            POLCSHIHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFEKQF
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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TISSUE=Testis;
Bloecker H., Boecher M., Brandt P., Mewes H.W., Gassenhuber
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GO:0016020; C:membrane; IEA.
GO:0004888; F:transmembrane receptor activity; IEA.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
101-MAX-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp434N1928 (Fragment).
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Submitted (NOV-1999) to the
EMBL; AL133097; CAB61408.1;
PIR; T42695; T42695.
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SEQUENCE 564 AA; 6
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                                                                                           NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 300
                                                                                                                   RKKQQENIYSHLDEESSESTYTAALPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAYFL 360
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01-MAR-2004 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
86f protein (Fragment).
Name=SEF;
Gallus gallus (Chicken).
Ebuaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVGPASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVTILMSPGA
PRNLNISQHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTETTSCLLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Facial mesenchyme;
MEDLINE=22651784; PubMed=12765832; DOI=10.1016/S0968-0004(03)00067-7;
Novatchkova M., Leibbrandt A., Werzowa J., Neubueser A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The STIR-domain superfamily in signal transduction, development
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Trends Biochem. Sci. 28:226-229(2003).
EMBL, AJS08679; CAD48485.1;
GO; GO:0016020; C:membrane; IEA.
GO; GO:0004888; F:transmembrane receptor activity; IEA
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Matches 528; Conserv
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NCBI_TaxID=9031;
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01-MAR-2003 (
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08AV76
10 AND 1-M
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                                 LGIEFLKGFRVILEELKSEGRQCQQLILKDPRQLNSSFKRTGMESQPFLNMKFETDYFVK
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2004 (TrEMBLrel. 26, Last annotation update)
101-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Interleukin 17 receptor-like protein short form.
Name=1117rd, Synonyms=1117rlm,
Man musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria; Rodentia; Sciurognathi; Muridae; Muxinae; Muscula: LaxID=10090;
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PubMed=12958313; DOI=10.1074/jbc.M306936200;
Xiong S., Zhao, Q., Rong Z., Huang G., Huang Y., Chen P., Zhang Liu L., Chang Z.,
Thibibite PC-12 cell differentiation by interfering with F mitogen-activated protein Kinase MAPK signaling.";
J. Biol. Chem. 278:50273-50282(2003).
Biol. Chem. 278:50273-50282(2003).
MGD; MGI:2159727; Ill7rd.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005634; C:nucleus; IEA.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2004 (TrEMBLrel. 26, Last annotation update)
Similar expression to FGF protein (Fragment).
Name=1117td; Synonyme=Sef;
Nus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                              69.9%; Score 2675.5; DB 2; Length 594;
84.8%; Pred. No. 1.8e-194;
ive 34; Mismatches 50; Indels 7;
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BEDILNE-2182423; PubMed=11802165; DOI=10.1038/ncb750;
Furthaue.z. M., Lin W., Ang S.L., Thisse B., Thisse C.;
"Sef is a feedback-induced antagonist of Ras/MAPK-mediated
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004888; F:transmembrane receptor activity; IEA.
GO; GO:0008270; F:zinc ion binding; IEA.
InterPro; IFR000157; TIR.
InterPro; IPR007087; Znf_C2H2.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
                                                             594 AA; 66780 MW; EABE6B655DCF4EC3 CRC64;
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Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
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                                               MGD; MGI:2159727; III7Td.

RGG; GO:0016020; C:nembrane; IEA.

RGG; GO:0005674; C:nucleus; IEA.

RGG; GO:0003676; F:nucleus; IEA.

RGG; GO:0003676; F:nucleus; IEA.

RGG; GO:0004888; F:transmembrane receptor activity; IEA.

RGG; GO:0004888; F:transmembrane receptor activity; IEA.

RGG; GO:0004888; F:transmembrane receptor activity; IEA.

RGG; GO:0004888; F:transmembrane receptor activity; IEA.

RGG; GO:0004888; F:transmembrane receptor activity; IEA.

RGG; GO:0004888; F:transmembrane receptor activity; IEA.

RGG; GO:0004888; F:transmembrane receptor activity; IEA.

RGG; GO:0004888; F:transmembrane receptor activity; IEA.

RGG; GO:0004888; F:transmembrane receptor activity; IEA.

RGG; GO:0004888; F:transmembrane receptor activity; IEA.

RGG; GO:0004888; F:transmembrane receptor activity; IEA.

RGG; GO:0004888; F:transmembrane receptor activity; IEA.
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Last annotation update)
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Nat. Cell Biol. 4:170-174(2002)
EMBL; AF424804; AAL79530.1; -.
MGD; MGI:2159727; Ill7rd.
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-MAR-2004 (TrEMBLrel. 26,
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                                                                                                                                                                            50.9%; Score 1950.5; DB 2; Length llarity 54.1%; Pred. No. 3.1e-139; Conservative 106; Mismatches 184; Indels
[1]
SEQUENCE FROM N.A.
MEDLINE=21824236; PubMed=11802164; DOI=10.1038/ncb749;
MEDLINE=21824236; PubMed=11802164; DOI=10.1038/ncb749;
Tang M., Friesel R., Kudoh T., Dawid I.;
"Identification of Sef, a novel modulator of FGF signa"
Nat. Cell Biol. 4:165-169(2002).
EMBL; AF364103; AAL76112.1; -.
SENIX ZBB-GENE-02320-5; ill7rd.
SEQUENCE 745 AA; 83431 MW; 56FE1F0B9D98DDB4 CRC64;
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01-07N-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
FGF signaling antagonist Sef.
Name=illTd; Stragonist Sef.
Brachydanio rerio (Zebrafish) (Danio rerio).
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 Vertebrata; Euteleostomi;
Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                  35;
                                                                                                                                       FGF
                                                                                                                                                                                                                                                                                                                                  2; Length 745;
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MEDLINE=21824237; PubMed=11802165; DOI=10.1038/ncb750;
Furthauer M., Lin W., Ang S.L., Thisse B., Thisse C.;
"Sef is a feedback-induced antagonist of Ras/MAPK-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMEGLSTDOTETSSLTESVSSSSGLGEEEPPALPSKLLSSGS-CKADL
                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   544 VPFHPPPLRYREPVLEKFDSGLVLNDVMCKPGPESDFCLKVEAAVL-
                                                                                                                                                                                                                        Fuerthauer M., Lin W., Siew-Lan A., Thisse B., Thisse C. Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AF401232; AAL78817.1; -. ZEN, ZDB-GENE-020320-5; ill7rd.
                                                                                                                                                                                                                                                                                                745 AA; 83437 MW; 75BB9EDCC08A4652 CRC64;
                                                                                                                                                                                                                                                                                                                              50.7%; Score 1941.5; DB 2;
ilarity 53.8%; Pred. No. 1.5e-138;
Conservative 108; Mismatches 184;
Eukaryota, Metazoa, Chordata, Craniata,
Actinopterygii, Neopterygii, Teleostei,
                                                                                                                                                                           Nat. Cell Biol. 4:170-174(2002)
                                                                                                                                                                                                                                                                                                                                                    Similarity
                                     Danio.
                                                                                                                                                                                           [2]
SEQUENCE FROM N.A.
                                    Cyprinidae, Dani
NCBI TaxID=7955;
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Transmembrane.
                                                                                                                                                                                                                                                                                   gnaling
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                           81
                                                                                                                                                      TISSUE-Frontal lobe left;
MEDLINE=21458551; PubMed=11574149; DOI=10.1016/S0378-1119(01)00665-5;
Osada M., Hida M., Kusuda J., Tanuma R., Iseki K., Hirata M., Suto Y.,
Hirai M., Terao K., Suzuki Y., Sugano S., Hashimoto K.;
"Assignment of 118 novel cDNAs of cynomolgus monkey brain to human
                                                                                                                                                                                                                                                                                                                                                                                     1 ADTCGWRMKAAARPRLCVANEGVGPASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNI
                                                                                                                                                                                                                                                                                                                                                                                                  36 ADTCGWR------GVGPASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNI
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                 Hypothetical protein. Macaca fascicularis (Cynomolgus monkey). Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yao Z., Spriggs M.K., Derry J.M.J., Strockbine L., Park L.S., Vanden Bos T., Zappone J., Painter S.L., Armitage R.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=T-cell;
MEDLINE=98035683; PubMed=9367539; DOI=10.1006/cyto.1997.0240;
                                                                                                                                                                                                                                                                                                                                          Length 109;
                                                                                                                                                                                                                                                                                                                                        9.2%; Score 354; DB 2; Length 10
81.7%; Pred. No. 4.3e-19;
iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

TISSUE=Frontal lobe left;
Hashimoto K., Osada N., Hida M., Kusuda J., Sugano S.;
Submitted (CT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AB093642; BAC21616.1; -...
                                                                                                                                                                                                                                                                                                                    109 AA; 11609 MW; 7EB13B49DB4C925B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         096746; 043844;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Interleukin-17 receptor precursor (IL-17 receptor).
                                            01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                866 AA
           109 AA
                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISQYACHDQVAVTILWSPGVL 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                  TISQYACHDQVAVTILWSPGAL 82
                                  (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                          Query Match 9.2
Best Local Similarity 81.7
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytokine 9:794-800(1997)
           PRELIMINARY;
                                                                                                               Cercopithecinae; Macaca.
                                                                                                                                                                                                                            Gene 275:31-37(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                          NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vanden Bos T
                                  01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=IL17R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                          82
                                                                                                                                                                                                                                                                                                                     SEQUENCE
                      овнхев;
            Q8HXE8
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brapleton M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C., A. Raha S.S., Loquellano M.A., Peters G.J., Abramson R.D., Mullahy S.J., Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., A. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., W. Villalon D.K., Muzny D.W., Sodergen B.J., Lu X., Gibbs R.A., Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., A. Rodriguez A.C., Grimwood J., Schwutz J., Myers R.M., Schein J.B., Schmutz J., Myers R.M., Schein J.B., Jones S.J.M., Marra M.A., Schein J.B., Jones S.J.M., Marra M.A., Schein J.B., Jones S.J.M., Marra M.A., Schein J.B., Jones S.J.M., Marra M.A., Schein J.B., Jones S.J.M., Marra M.A., Schein J.B., Jones S.J.M., Marra M.A., Schein J.B., Jones S.J.M., Marra M.A., Schein J.B., Jones S.J.M., Marra M.A., Schein J.B., Jones S.J.M., Marra M.A., Schein J.B., Jones S.J.M., Marra M.A., Schein J.B., Jones S.J.M., Marra M.A., Schein J.B., Jones S.J.M., Marra M.A., Schein J.B., Jones S.J.M., Marra M.A., Schein J.B., Jones S.J.M., Marra M.A., Schein J.B., Jones S.J.M., Marra M.A., Schein J.B., Jones J.M., Marra M.A., Schein J.B., Jones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78
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GO: GO:0030368; F:interleukin-17 receptor activity; NAS.
GO: GO:0007166; P:cell surface receptor linked signal transdu. . .; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Verified cleavage sites.";
Verified cleavage sites.";
Protein Sci. 13:2819-2824(2004).
-!- FUNCTION: Receptor for IL17. Binds its ligand with low affinity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 NITPKYDNC--TTYLNPVGKHVIADAQNIT-----ISQYACHDQ-----VAVTILWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49 NCTVKNSTCLDDSWIHP------RNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- SUBCELLUTAR LOCATION: Type I membrane protein (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
8.1%; Score 310; DB 1; Length 866;
Best Local Similarity 23.1%; Pred. No. 1.7e-14;
Matches 178; Conservative 107; Mismatches 338; Indels 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=15340161; DOI=10.1110/ps.04682504;
Zhang Z., Henzel W.J.;
"Signal peptide prediction based on analysis of experimentally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct protein sequencing; Glycoprotein; Receptor; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interleukin-17 receptor.

Extracellular (Potential).

Cytoplasmic (Potential).

Poly-Glu..

N-linked (GlCNAC...) (Pot.

N-linked (GlCNAC...) (Pot.

N-linked (GlCNAC...) (Pot.

N-linked (GlCNAC...) (Pot.

N-linked (GlCNAC...) (Pot.

N-linked (GlCNAC...) (Pot.

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N-linked (GlCNAC...) (Pot.

N-linked (GlCNAC...) (Pot.

N-linked (GlCNAC...) (Pot.

N-linked (GlCNAC...) (Pot.

V -> A (in Ref. 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   V -> A (in Ref. 1)
H -> R (in Ref. 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U58917; AAB99730.1; -.
EMBL; BC011624; AAH11624.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96131 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genew; HGNC:5985; IL17R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H-InvDB; HIX0016207; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- PTM: Glycosylated.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 33-47
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: : : : : : : : : : : : : : : : :	3 YFVKVVPFPSIKNESNYHPFFFRTRACDLILQPDNLACKPFWKPRNL 184	7 YEVTVHHIPKRIPDGDPNHQSKNFLVPDCEHARMKVTTPCMSSGSLWDP-NITVETLEAH 215	5 NISQHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTETT 235	216 QLRVSFTLWNESTHYQILLTSFPHMENHSCFEHMH-HIPAPRPEEFHQRSNVTLTLRNLK 274	5 SCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 292	275 GCCRHQVQIQPFFSSCLNDCLRHSATVSCPEMPDTPEPIPDYMPLMVYWFITGISILLVG 334	3 ATLFTUMCRKKQQENIYSHLDEESSESSTYTAALPRERLRPRPKVFLCYSSKDGQN 348	S SVILLIVCMTWRLAGPGSEKYSDDTKYTDGLPVADLIPPPLKPRKVWIIYSA-DHPL 390	9 HMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQKIHESQFIIVVCSKG 404	391 YVDVVLKFAQFLLTACGTEVALDLLEEQAISEAGVMTWVGRQKQEMVESNSKIIVLCSRG 450	5 MKYFVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIA 456	1 TRAKWQALLGRGAPVRLRCDHGKPVGDLFTAAMNMLLPDFKRPACFGTYVV 501		2 CYFSEVSCDGDVPDLFGAAPRYPLMDRFEEVYFRIQDLEMFQPGRMHRVGELSGDNYL 559	4 RSKSGRSLYVAICNMHQFIDEEPDWFEKQFVPFHPPPLRYREPVLEKFDSGL 565	0 RSPGGRQLRAALDRFRDWQVHCPDWFECENLYSADDQDAPSLDEEV-FEEPLLPP-GTGI 617	6 VINDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGG 605	618 VKRAPLVRE-PGSQACLAIDPLVGEEGGAAVAKLEPHLQPRGQPAPQPLHTLVLAAEEGA 676	606 IDQDGBARPALDGSAALQPLLHTVKAGSPSDMPRDSGIYDSSVPSSELSLP 656	677 LVAAVEPGPLADGAAVRLALAGEGEACPLLGSPGAGRNSVLFLPVDPEDSP 727	IMBGLSTDQTETSSLTESVSSSGLGEEEPPALPSKLLSSGSCKADLGC 705	8 LGSSTPMASPDLLPEDVREHLEGLWLSLFEQSLSCQAQGGC 768
100	138	157	185	216	236	275	293	335	349	391	405	451	457	502	514	260	995	618	909	677	657	728
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Search completed: August 9, 2005, 11:48:54 Job time : 117.24 secs